

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 1, 2004, 14:43:07 ; Search time 36 Seconds

(without alignments)
2.390 Million cell updates/secTitle: US-10-029-345a-109
Perfect score: 3418
Sequence: 1 MAHEMIGTQIVTERLVALLE.....LGRVGSQSSFSGSGMERIEVS 665Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 15 seqs, 64690 residues

Total number of hits satisfying chosen parameters: 30

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 15 summaries

Command line parameters:
-MODE=frame_plus_p2n.model -DEV=soft
-Q-Pending_Patents_MA.Main:US-10-029-345a-109 -DB=ring109.seq -SUFFIX=pto
-OUT=US-10-029-345a-109.rng -MINMATCH=0.1 -LOOPEXT=0 -UNITS=bits
-STAR=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=15 -DOCALLIGN=200
-THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pro
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -NCPU=6 -NO_XLPHY
-NEG SCORES=0 -LONGLOG -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YAFOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: ring109.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3406	99.6	5145	1 ABV21312	Human prostate exp
2	3406	99.6	5145	1 ABV21316	Human prostate exp
3	3406	99.6	5145	1 ABV26826	Human prostate exp
4	3406	99.6	5145	1 ABV27121	Human prostate exp
5	3406	99.6	5145	1 ABV26922	Human prostate exp
6	3406	99.6	5145	1 ABV27135	Human prostate exp
7	3406	99.6	5145	1 ABV28657	Human prostate exp
8	3406	99.6	5145	1 ABV22827	Human prostate exp
9	3406	99.6	5145	1 ABV26934	Human prostate exp
10	3398	99.4	2102	1 ADA53105	Human coding seque
11	3388	99.1	5111	1 AAH96855	Human protein enco
12	3388	98.7	2118	1 ACC60521	Polynucleotide rel
13	3057.5	89.5	2756	1 AAF30479	Human protein phos
14	3057.5	89.5	2756	1 ACC60560	Polynucleotide rel
15	3048.5	89.2	3332	1 ABK48378	CDNA encoding huma

ALIGNMENTS

RESULT 1

ID	ABV21312	ABV21312 standard; cDNA; 5145 BP.
XX	XX	ABV21312.
AC	XX	13-SEP-2002 (first entry)
DT	XX	Human prostate expression marker cDNA 21303.
DE	XX	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW	XX	pharmacogenomic marker; gene; ss.
XX	XX	Homo sapiens.
XX	XX	MO200160860-A2.
PN	XX	23-AUG-2001.
PD	XX	20-FEB-2001; 2001MO-US005171.
XX	XX	17-FEB-2000; 2000US-0183119P.
PF	XX	16-MAR-2000; 2000US-0189862P.
PR	XX	25-MAY-2000; 2000US-0207454P.
PR	XX	09-JUN-2000; 2000US-0211314P.
PR	XX	18-JUL-2000; 2000US-0219007P.
PR	XX	13-DEC-2000; 2000US-0255281P.
PA	XX	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PI	XX	Schlegel R, Endege WO, Monahan JB,
DR	XX	WPI; 2001-662795/76.
XX	XX	Novel isolated nucleic acid molecule associated with cancerous state of
PT	XX	prostate cells and correlating with presence of prostate cancer, useful
PT	XX	for detecting presence of prostate cancer, stage of prostate cancer.
PS	XX	Claim 1, Page 3539, 11750pp; English.
CC	XX	The invention relates to an isolated nucleic acid molecule (I) comprising
CC	XX	a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC	XX	specification or its complement. (I) is useful for: (a) assessing whether
CC	XX	a patient is afflicted with prostate cancer; (b) monitoring the
CC	XX	progression of prostate cancer in a patient; (c) assessing the efficacy
CC	XX	of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC	XX	the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC	XX	(e) selecting a composition for inhibiting prostate cancer in a patient;
CC	XX	(f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC	XX	determining whether prostate cancer has metastasized in a patient; (h)
CC	XX	assessing the aggressiveness or indolence of prostate cancer in a patient
CC	XX	; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
SQ	XX	Sequence 5145 BP; 1408 A; 1135 C; 1253 G; 1346 T; 0 U; 3 Other;
Alignment Scores:		
Pred. No.:	0	Length: 5145
Score:	3406.00	Matches: 663
Percent Similarity:	99.85%	Conservative: 1
Best Local Similarity:	99.70%	Mismatches: 0
Query Match:	99.65%	Gaps: 0
DB:	1	
US-10-029-345a-109 (1-665) x ABV21312 (1-5145)		
QY	1	MetAlHhIGlUwctllleglyThrGlnllvalThrGluArgLeuValAlaLeuLeuGln 20
DB	589	ATGGCCCATGAGATGATTGCACTCAATTGTACTGAGAGGTGGGCTCTGCTGGAA 648
QY	21	SerGlyThrGlnuValLeuLeuLlLeaPSeArqProPhaValGluTyraAntTrser 40
DB	649	AGTGAACGGAAGAAAGTGTCTTAATTGATGAGCGGCAATTGTGGATACATACATCC 708
QY	41	HisIleuGluAlaIleAsnIleAsnCySerIleuMetIysArgArgLeuGlnGln 60

Db 709 CACATTTGGAGGACATTATATCACTGCTCAAGCTTATGAAGGAGTTGCAACAG 768
Qy 61 AspLysValLeuIleThrGluLeuIleGlnHisSerAlaLysHisLysValAspIleAsn 80
Db 769 GACAAAGCTTATATACAGAGCTCATCCAGCATTCAGGAAACATTAAGGTGACATTTAT 828
Qy 81 CysSerGlnLysValValValLysAspGlnSerSerGlnAspValAlaSerLeuSer 100
Db 829 TGCACTGAGAAAGTTGTAGTTTACAGATCAAAAGCTCCAAAGATGTTGCTCTCTCTCA 888
Qy 101 AspCysPheLeuThrValLeuLeuGlyLysLeuGlyLysSerPheAsnSerValHisLeu 120
Db 889 GACTGTTTCTCAGCTACTCTCTGGGTAAACTGGAGAAAGAGCTCAACTCTGTTCACTGG 948
Qy 121 LeuAlaGlyLysPheAlaGluPheSerArgCysPheProGlyLeuCysGluGlyLysSer 140
Db 949 CTTCAGAGTGGGTTCGTGAGTTCTCTGTTGTTTCCCTGGCTCTGTGAAGGAAATCC 1008
Qy 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
Db 1009 ACTTAGTCCCTACCTGACATTTCTCAGCTTGTCTTACCTGTTGCCAATTTGGGCAAC 1068
Qy 161 ArgIleLeuProAsnLeuTyrLeuGlyCysGlnArgAspValLeuAsnLysGluLeuIle 180
Db 1069 CGAATTCCTCCCAATCTTATCTTGGCTGCCAGCAGATGTCCTCAACAGAGCTGATG 1128
Qy 181 GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyrThrCysProLysProAspPhe 200
Db 1129 CAGCGAATGGGATTTGTTATGTTTAATGCCAAATACCTGTCGCAACCTCGACTTT 1188
Qy 201 IleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGluLysIleLeu 220
Db 1189 ATCCCGAGTCTCATTTCTCTGCTGCTGCTGATGATGACAGCTTTTGGAGAAATTTTG 1248
Qy 221 ProTrpLeuAspLysSerValAspPheIleGlyLysAlaLysAlaSerAsnGlyCysVal 240
Db 1249 CCGGTGTGGCAATCGATGATTTCAATTGAGAAAGCAAAAGCTCCAAATGATGCTT 1308
Qy 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
Db 1309 CTAGTGCACTTTTAGCTGGAGATCTCCGCTCCGCCACCACTGCTATGCTTACATCATG 1368
Qy 261 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLysArgProThr 280
Db 1369 AAGGAGATGACATGCTTTAGATGAGCTTACAGATTTGGAAGAAAGAAAGACTTACT 1428
Qy 281 IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGlyLysLysIleLysAsn 300
Db 1429 ATATCTCCAAACTTCAATTTCTGGGCCACTCTGACATATGAGAAAGATTTAAGAAC 1488
Qy 301 GlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuHisLeuGluLysProAsn 320
Db 1489 CAGACTGGAGACTCAGGGCCAAAGAGCAAACTCAAGCTGCTGACCTGGAGAAACCAAT 1548
Qy 321 GluProValProAlaValSerGluGlyLysGlnLysSerGlnThrProLeuSerProPro 340
Db 1549 GAACCTGTCCCTGCTGCTCAGAGGTGACAGAAAGAGGAGCGCCCTCAGTCCACCC 1608
Qy 341 CysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisProAlaSerVal 360
Db 1609 TGTGCCACCTCTGTACTCTCAGAGGACAGCAAGAAAGCCCGGACATCCCGCAGCGTG 1668
Qy 361 ProSerValProSerValGlnProSerLeuGluLysAspSerProLeuValGlnAlaLeu 380
Db 1669 CCGAGCGTCCGACCGTGCAGCCCTCTGTTAAGACAGACCCGCTGGTACAGGCCCTC 1728
Qy 381 SerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLysArgSerPhe 400
Db 1729 AGTGGCTGCACCTGTCGCGACAGAGCTGGAAGACATTAAGCTCAAGCGTTCTTTC 1788
Qy 401 SerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPhe 420

Db 1789 TCTCTGATATCAATACATTCATATTCAGCCAGCATGCGAGCATCTTACATGCTTC 1848
Qy 421 SerSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAspGlyThrAsn 440
Db 1849 TCTCATCAAGAGTGTCTTGGATTAAGTACTACAAACTTCCACTCTGTGATGGGACCAAC 1908
Qy 441 LysLeuCysGlnPheSerProValGlnLysSerGluGlnThrProGluThrSerPro 460
Db 1909 AAGCTTAGCCAGTTCTCCCTCTGTTACAGGAATTCGAGAGAGACTCCCGAAACAGCTC 1968
Qy 461 AspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSerAspSerGln 480
Db 1969 GATTAAGAGAGAGCAGCATCCCAAGAACTCAGACCCCGAGGCTTTCAGACAGCAG 2028
Qy 481 SerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500
Db 2029 AGCAAGCAATTCATTCGTGAGAAACAGACAGATGTCACCCGCCAGAGGCTCCCTTTA 2088
Qy 501 SerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheGly 520
Db 2089 TCTCCTCATGCAATGGAAGTGGAGCGTGAAGACATTAACACACAGCTTCTTTTCGCG 2148
Qy 521 LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLysGlyTyrPheHis 540
Db 2149 CTTTCCACGACGACGACACTCAGCAAGTCTGCTGGGCTTAAAGGCTGGCAC 2208
Qy 541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPheAla 560
Db 2209 TCGGATATCTTGGCCCCCAGACCTTACCCCTTCCCTGACAGCAGCTGTGATTTTGGC 2268
Qy 561 ThrGlnSerSerHisPheTyrSerAlaSerAlaIleTyrGlyLysSerAlaSerTyrSer 580
Db 2269 ACAAGATCTCAACACTTCTACTCTGCTCAGCATCTAAGGAGCGATGCCACTTACTCT 2328
Qy 581 AlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValLysSerValArgArgArg 600
Db 2329 GCCTTACAGCTGACGCGACGCTCCACTTGGGAGACCAAGTCTTATCTGTGCGCAGCGG 2388
Qy 601 GlnLysProSerAspArgAlaAspSerArgArgSerTriHisGluGlnSerProPheGlu 620
Db 2389 CAGAGCGCAAGTACAGAGCTGACTGCTGGCGGAGCTGGCATAAAGAGCCCTTTGAA 2448
Qy 621 LysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerIleMetSerGluAsn 640
Db 2449 AAGCAGTTTAAAGCAGAGAGCTCCAAATGGAATTTGAGAGAGCATCATGTCAAGAAC 2508
Qy 641 ArgSerArgGluLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetGlu 660
Db 2509 AGGTCAAGGAGAGAGCTGGGAGAAAGTGGCAAGTCTTATCTTTCGGGCGACATGAA 2568
Qy 661 IleIleGluValSer 665
Db 2569 ATCATTTAGGTTCTCC 2583
RESULT 2
ABV21316
ID ABV21316 standard; cDNA; 5145 BP.
XX
AC ABV21316;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 21307.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN NC200160860-A2.
XX
PD 23-APR-2001.
XX

PF 20-FEB-2001; 2001MO-US005171.
XX
PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
XX MPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 3540; 11750DP; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABY00010-ABY62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 5145 BP; 1408 A; 1135 C; 1253 G; 1346 T; 0 U; 3 Other;

Alignment Scores:
Pred. No.: 0 Length: 5145
Score: 3406.00 Matches: 663
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.70% Mismatches: 0
Query Match: 99.65% Indels: 0
DB: 1 Gaps: 0

US-10-029-345a-109 (1-665) X ABV21316 (1-5145)
QY 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluLeuValAlaLeuLeuGlu 20
DB 589 ATGGCCCATGAGATGATGAGACTCAATGTTACTGAGAGGTTGGCTGCTGGGAA 648
QY 21 SerGlyThrGlyValLeuLeuLeuIleAspSerArgProPheValGluTyrAsnThrSer 40
DB 649 AGTGAACGAAAGAGTGTCTTAATTGATAGCGGCGCATTTGGAGATACAAATACATCC 708
QY 41 HisIleLeuGlnAlaIleAsnIleAsnGlySerLeuMetCysArgArgLeuGln 60
DB 709 CACATTTTGAACCATTAATATCACTGCTCAAGTTATGAAGCAAGAGTTGCAACAG 768
QY 61 AspLeuValLeuIleThrGluLeuIleGlnHisSerAlaValHisLeuValAsp 80
DB 769 GACAAAGTGTAAATTCAGAGCTCATCCACATTCAGCGAAACATAGCTTGACATTGAT 828
QY 81 CysSerGlnLeuValValValTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
DB 829 TGCAGTCAGAAAGTTGATTTACGATCAAGCTCCCAAGATGTGCTCTCTCTTCA 888
QY 101 AspCysPheLeuThrValLeuLeuGlyValLeuGlyValSerPheAsnSerValHisLeu 120
DB 889 GACGTGTTTCTCACTGACTTCTGGGTAACCTGGAGAAAGACTTCACTGTTCACTG 948
QY 121 LeuAlaGlyValPheAlaGluPheSerArgCysPheProGlyLeuCysGlyGlyValSer 140
DB 949 CTTCGAGGTGGTGGTTCGATGTTCTCTGTTGTTCCCTGGCCTGTGTGAAGAAATCC 1008

QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
DB 1009 ACTCTAGTCCCTTACCTGATTTCTGACCTTGTTCATCTGTTGCCAAATGGGCCAAC 1068
QY 161 ArgIleLeuProAsnLeuTyrLeuGlyCysGlnArgAspValLeuAsnGlyLeuIle 180
DB 1069 CGAATTCCTCCCAATCTTATCTTGGCTGCGACGAGATGCTCTCAACAGAGAGCTGATG 1128
QY 181 GlnGlnAsnGlyTyrIleGlyTyrValLeuAsnAlaSerTyrThrCysProValProAspPhe 200
DB 1129 CAGCAAAATGGAGTTGATTATGTTAAATGCGAGCAATACCTGTCAAAGCTGACTTT 1188
QY 201 IleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGlyValIleLeu 220
DB 1189 ATCCCGAGTCTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1248
QY 221 ProTyrLeuAspIleSerValAspPheIleGlyValAlaValAsnGlyCysVal 240
DB 1249 CCGTGGTTGGACAAATCAGTATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1308
QY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
DB 1309 CTAGTCCACTGTTTACTGAGATCTCCCTCCGCAACATGCTATCGCTACATCATG 1368
QY 261 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValIleGlyValArgProThr 280
DB 1369 AAGAGATGAGACATGCTTATGATGAAGCTTACAGATTTGTGAAGAAAGAAACCTACT 1428
QY 281 IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGlyValIleValAsn 300
DB 1429 ATATCTCCAAACTTCATTTTCTGGGCGCAACTCTGACTATGAGAAAGATTAAGAAC 1488
QY 301 GlnThrGlyAlaSerGlyProLysSerIleLeuLeuLeuHisIleGlnIleValProAsn 320
DB 1489 CAGACTGGAGCATCAGAGCGCAAGAGCAAACTCAACTGCTGAGCCGAGGAGCAAAAT 1548
QY 321 GluProValProAlaValSerGlyGlyGlnIleSerGlyThrProLeuSerProPro 340
DB 1549 GAACCTGCTCCCTGCTCTTCAAGAGGTGAGCAAGAAAGGAGCGCCCTCATCCACCC 1608
QY 341 CysAlaAspSerAlaThrSerGlnAlaIleGlyGlnArgProValHisProAlaSerVal 360
DB 1609 TGTGCCGACTGCTCTACTCAGAGCAGAGCAAGAGCGCCGTGATCCCGCAGCGTG 1668
QY 361 ProSerValProSerValGlnProSerLeuLeuGlnAspSerProLeuValGlnAlaLeu 380
DB 1669 CCGAGGTGCCCAAGCGCTGAGCGGTGTTAGAGAGACGCCGCTGTACAGCGCTC 1728
QY 381 SerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnIleValArgSerPhe 400
DB 1729 AGTGGCTGACCTGCTCCGACAGAGCTGGAAGACAGCAATAGCTCAAGCTTCTTC 1788
QY 401 SerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPhe 420
DB 1789 TCTCTGATATCAATCAATGATTCATATTCAGCAGCATGGCAGCATCTTACATGGCTTC 1848
QY 421 SerSerSerGlnAspAlaLeuGlyTyrTyrIleProSerThrThrLeuAspGlyThrAsn 440
DB 1849 TCTCTCATCAGAAATCTTGGAAATCTCAAACTTCCATCTGTGATGGAGCAAC 1908
QY 441 LysLeuCysGlnPheSerProValGlnIleLeuSerGlnIleThrProGluThrSerPro 460
DB 1909 AAGCTATGCCAGTCTCCCTGTTCAAGAACTATCGAGAGAGCTCCCAAGAACAGCTCT 1968
QY 461 AspLeuGlnGluAlaSerIleProLysValLeuGlnThrAlaArgProSerAspSerGln 480
DB 1969 GATTAAGAGAGAGCCAGATCCCAAGAGAGCTGCAACCGCGCTTCAAGACAGCAG 2028
QY 481 SerTyrArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500
DB 2029 AGCAAGCGATTCGATTCGATCAGAACCAAGAGAGAGCGCCCAAGAGAGCTCTTTTA 2088

QY 501 SerProLeuHisArgSerGlySerValGluAspAenTyRHisThrSerPheLeuPheGly 520
Db 2089 TCTCCACCTGCATCGAAGTGGGAGCGGTGGAGGACAAATTACCAACAGCTTCCTTTCCGAC 2148
QY 521 LeuSerThrSerGlnHisIleuThrIysSerAlaGlyLeuGlyLeuLysGlyTyrHis 540
Db 2149 CTTTCACCGACGACAGCACTCAAGAGTGTGCTGGCTGGGCTTAAAGGAGCTGGGAC 2208
QY 541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPheAla 560
Db 2209 TCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCTGACACAGCAGCTGGATTTTCC 2268
QY 561 ThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAlaSerTyrSer 580
Db 2269 ACAGAGTCTTCACTTCTACTCTCTCCCTCAGCCATCTACGAGGAGGAGTCCAGTTACTCT 2328
QY 581 AlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArgArg 600
Db 2329 GCTTACAGCTGACGACGCTGCCCTTGCAGGAGCAAGTCTATTCTGTGCGGAGGCGG 2388
QY 601 GlnLysProSerAspArgAlaAspSerArgArgSerTyrPheGlnGluSerProPheGln 620
Db 2389 CAGAAAGCAAGTGAAGAGAGTGAATCTCGCGCGAGCTGGCATGAAGAGACCCCTTTGAA 2448
QY 621 LysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerTyrMetSerGluAsn 640
Db 2449 AAGCAGTTTAAACGACGAAGCTGCCAAATGGAAATTTGAGAGAGCATCATGTACAGAAC 2508
QY 641 ArgSerArgGlnGluLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetGlu 660
Db 2509 AGCTACCGGGAAGAGCTGGGGAAGTGGGAGTCACTGCTTCTTTCGGGACGATGAA 2568
QY 661 IleIleGluValSer 665
Db 2569 ATCATTTGAGGTCTCC 2583

RESULT 3

ABV26826
ID ABV26826 standard; cDNA; 5145 BP.

XX AC ABV26826;
XX 16-SEP-2002 (first entry)
XX Human prostate expression marker cDNA 26817.
XX DE Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX MO200160860-A2.
XX 23-AUG-2001.
XX 20-FEB-2001; 2001WO-US005171.
XX 17-FEB-2000; 2000US-0183319P.
XX 16-MAR-2000; 2000US-0189862P.
XX 25-MAY-2000; 2000US-0207454P.
XX 09-JUN-2000; 2000US-0211314P.
XX 18-JUL-2000; 2000US-0219007P.
XX 13-DEC-2000; 2000US-0255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.

XX Claim 1; Page 5420-5421; 11750bp; English.
PS The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing whether prostate cancer has metastasized in a patient; (g)
CC determining the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
50 Sequence 5145 BP; 1408 A; 1135 C; 1253 G; 1346 T; 0 U; 3 Other;
Alignment Scores:
Pred. No.: 0 Length: 5145
Score: 3406.00 Matches: 663
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.65% Indels: 0
DB: 1 Gaps: 0
US-10-029-345a-109 (1-665) x ABV26826 (1-5145)
QY 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGlu 20
Db 589 ATGGCCCATAGATGATGTGGAACCTCAAAATTTGTATCTGAGAGGTGTGGCTCGCGGAA 648
QY 21 SerGlyThrGlnLysValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
Db 649 AGTGGAAAGGAAAGAGTGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 708
QY 41 HisIleLeuGluAlaIleAsnIleAsnCysSerLysLeuMetLysArgArgLeuGlnGln 60
Db 709 CACATTTTGGAAAGCATTAATATCACTGCTCCAACTTATGAAGGAGGATGGAACAG 768
QY 61 AspLysValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
Db 769 GACAAAGTGTAAATACAGAGCTCATTCAGCATTCAGCAAAATGAAGTGTGACATTGAT 828
QY 81 CysSerGlnLysValValTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
Db 829 TGAAGTCAGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 888
QY 101 AspCysPheLeuThrValLeuLeuGlyLysLeuGluLysSerPheAsnSerValHisLeu 120
Db 889 GACTGTTTCTCACTGATCTTGGGTAACTGGAAGAGCTTCAACTCTGTTCACTG 948
QY 121 LeuAlaGlyLysPheAlaGluPheSerArgCysPheProGlyLeuCysGluGlyLysSer 140
Db 949 CTTCAGAGTGGGTTTCTGATGATCTCTGTTGTTCCCTGCGCTCTGTAAGGAAATTC 1008
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
Db 1009 ACTCTAGTCCCTACCTCGATTTCTGAGCTTCTGCTTACCTGTTGCCAACTTGGGCCAAC 1068
QY 161 ArgIleLeuProAsnLeuTyrLeuGlyCysGlnArgAspValLeuAsnLysGluLeuLeu 180
Db 1069 CGAATTCCTCCCAATCTTATCTTGGCTCCAGCGAGATGTCTCAACAAGAGGCTGANG 1128
QY 181 GlnGlnAsnGlyTyrIleGlyTyrValLeuAsnAlaSerTyrThrCysPheProAspPhe 200
Db 1129 CAGCAAGATGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1188
QY 201 IleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluLysIleLeu 220
Db 1189 ATCCCGGATCTCATTTCTGCGGTGCTGATGATGATGATGATGATGATGATGATGATGAT 1248
QY 221 ProTyrLeuAspLysSerValAspPheIleGluLysAlaLysAlaSerAsnGlyCysVal 240

```

Db      1249  CCCTGGTTGGACAATCATGATGATTTTCATTGAGAAAGCAAAAGCCTCATGATGATGTT 1308
Qy      241    LeuValHisGlyLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaIleAlaIleMet 260
Db      1309  CTAGTGACACTGTTAGCTGGGATCTCCGCTCCGCCCACTCCGCTATCGCTCATCATCATG 1368
Qy      261    LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValIleValGluLysArgProThr 280
Db      1369  AAGAGATGAGCAATGCTTTAGATGAAGCTTACGATTTGTGAAGAAAAAGAAAGCACTACT 1428
Qy      281    IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluIleValIleValAsn 300
Db      1429  ATATCTCCAACCTTCAATTTTCTGGGCCCAACTCCTGGACTATGAGAAAGATTAAGAAC 1488
Qy      301    GlnThrGlyValaSerGlyProLysSerIleLeuIleLeuIleLeuIleValIleValProAsn 320
Db      1489  CAGACTGAGCAATCAGGGCCAAAGAGCAAACTCAAGCTGTGCACTCGAAGAACCAAAAT 1548
Qy      321    GluProValProAlaValaSerGluGlyGlyIleValSerGluThrProLeuSerProPro 340
Db      1549  GAACCTGTCCCTCTGCTGTCTAGAGGGTGGACAGAAAAAGCAAGAGCCCTCATCTCACCC 1608
Qy      341    CysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisProAlaSerVal 360
Db      1609  TGTGCGACTGCTGCTACTCAGAGGACGACGACAAAGCCCGTGATCCCGCAGCGGTG 1668
Qy      361    ProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAlaLeu 380
Db      1669  CCGAGGTGCCCGCAGCGCCGTCGCTGTAGAGACAGCCCGCTGATACAGGCCCTC 1728
Qy      381    SerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLysValAspSerPhe 400
Db      1729  AGTGGGCTGCACCTGTCCGACAGAGCTGGAAGACAGCAATTAAGCTCAAGCCTTCTTC 1788
Qy      401    SerLeuAspIleLysSerValaSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPhe 420
Db      1789  TCTGTGATATCAAAATCATGATTTTATTTACGCCAGCATGGCAGATCTTACATAGGCTTC 1848
Qy      421    SerSerSerGluAspAlaLeuGluTyrTyrTyrLysProSerThrThrLeuAspGlyThrAsn 440
Db      1849  TCTCTATCAGAAATGCTTTGGAAATATCAAACTTCCACTCTCTGATGGGAGCCMAC 1908
Qy      441    LysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSerPro 460
Db      1909  AAGCTATGCCAGTCTCTCCCTGTTCAAGAACTATCGAGAGACTCCCGAAACCAAGTCTCT 1968
Qy      461    AspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSerAspSerGln 480
Db      1969  GATTAAGAGAGAACCCAGCATCCCAAGAAAGCTGCAAGCCGCAAGCCTTCAGACAGCCAG 2028
Qy      481    SerLysArgLeuHisSerValaArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500
Db      2029  AGCAACGATATGATTCGTGTCACAAACAGACAGAGTGGCACCCGCCAGAGGTCTCCCTTTTA 2088
Qy      501    SerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheGly 520
Db      2089  TCTCCACTGATGAACTGGAGGAGGCTGAGAGCAATTACACACCAAGCTTCTTTTGGGC 2148
Qy      521    LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLysGlyTyrHis 540
Db      2149  CTTTCCACCAAGCCAGACGACCTCAGCAAGTCTGTGCTGGGCTTAAAGGCTGGCAC 2208
Qy      541    SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrTyrPheAla 560
Db      2209  TCCGATATTCCTGGCCCCCAGACCTTACCCCTTCCCTGACAGCAAGCTGTATTTTGGCC 2268
Qy      561    ThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAlaSerTyrSer 580
Db      2269  ACGAGTCTCTACACTTCTACTCTGCTCAGCCATCTACGAGGAGGAGGACAGTACTCT 2328
Qy      581    AlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerValaArgArg 600

```

```

Db      2329  GCCTACAGCTGACCCAGCTGCCACTTGGCGAGACCAAGTCTATTCTGTGCGCAGCGG 2388
Qy      601    GlnLysProSerAspArgAlaAspSerArgArgSerThrHisGluGluSerProPheGlu 620
Db      2389  CAGAGCCAAATGATACAGAGCTGACTCGCGGAGCTGGGATGAGATGAAGAGACCCCTTGAA 2448
Qy      621    LysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerIleMetSerGluAsn 640
Db      2449  AAGCAGTTTAAACGAGAGAGCTCCAAATGGAATTTGGAGAGAGCATCATGTACAGAGAC 2508
Qy      641    ArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetGlu 660
Db      2509  AGGTCAAGGAGAGAGCTGGGGAAAGTGGGCAATCAGTCTGCTTTTCGGGACAGATGAA 2568
Qy      661    IleIleGluValSer 665
Db      2569  ATCATTAGGCTCTCC 2583

RESULT 4
ABV27131
ID  ABV27131 standard; cDNA; 5145 BP.
XX
AC  ABV27131;
XX
DT  16-SEP-2002 (first entry)
XX
DE  Human prostate expression marker cDNA 27122.
XX
KW  Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW  pharmacogenomic marker; gene; ss.
XX
OS  Homo sapiens.
XX
PN  M0200160860-A2.
XX
PD  23-AUG-2001.
XX
PF  20-FEB-2001; 2001MO-US005171.
XX
PR  17-FEB-2000; 2000US-0183319P.
PR  16-MAR-2000; 2000US-0189862P.
PR  25-MAY-2000; 2000US-0207454P.
PR  09-JUN-2000; 2000US-0211314P.
PR  18-JUL-2000; 2000US-0219007P.
PR  13-DEC-2000; 2000US-0255281P.
XX
PA  (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI  Schlegel R, Endege WO, Monahan JE;
XX
WPI; 2001-662795/76.
XX
DR  Novel isolated nucleic acid molecule associated with cancerous state of
PT  prostate cells and correlating with presence of prostate cancer, useful
PT  for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS  Claim 1; Page 5499-5500; 11750pp; English.
XX
XX
XX  The invention relates to an isolated nucleic acid molecule (I) comprising
XX  a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX  specification or its complement. (I) is useful for: (a) assessing whether
XX  a patient is afflicted with prostate cancer; (b) monitoring the
XX  progression of prostate cancer in a patient; (c) assessing the efficacy
XX  of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX  the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX  (e) selecting a composition for inhibiting prostate cancer in a patient;
XX  (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX  determining whether prostate cancer has metastasized in a patient; (h)
XX  assessing the aggressiveness or indolence of prostate cancer in a patient
XX  ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ  Sequence 5145 BP; 1408 A; 1135 C; 1253 G; 1346 T; 0 U; 3 Other;

```

Alignment Scores:

Pred. No.: 0 Length: 5145
Score: 3406.00 Matches: 663
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.65% Indels: 0
DB: 1 Gaps: 0

US-10-029-345a-109 (1-665) x ABV27131 (1-5145)

QY 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGlu 20
DB 569 ATGGCCCATGAGATATGGAACTCAAAATGTGTACTGAGAGGTGGTGGCTCTGCTGAA 648
QY 21 SerGlyThrGluValLeuLeuLeuIleAspSerArgProPheValGluTyrAsnThrSer 40
DB 649 AGTGAAGAGGAAAAAGTCTGCTAATTGATAGCCGGCAATTTGTGAATACAAATACATCC 708
QY 41 HisIleLeuGlnAlaIleAsnIleAsnCySerIlySleuMetLysArgArgLeuGln 60
DB 709 CACATTTGGAAAGCCATTAAATATCAATGCTCCCAAGCTTTATGAAAGCGAAGGTGCAACAG 768
QY 61 AspLysValLeuIleThrGluLeuIleGlnHisSerAlaLysIleValAspIleAsp 80
DB 769 GACAAAGGTAAATACAGAGCTCATCCAGCATTCAGGAAACATTAAGGTGACATTGAT 828
QY 81 CysSerGlnLysValValValTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
DB 829 TGGAGTCAGAAAGTTGATGTTTACATCAAAAGCTCCCAAGATGTTGCTCTCTCTTCA 888
QY 101 AspCyPheLeuThrValLeuLeuGluLysLeuGluLysSerPheAsnSerValHisLeu 120
DB 889 GACTGTTTTCACAGTACTCTGGGTAAACGTGGGAAAGACCTTCAACTCTGTTCACCTG 948
QY 121 LeuAlaGlyIlePheAlaGluPheSerArgCysPheProGlyLeuGlyLysSer 140
DB 949 CTTCAGAGTGGGTTTCTGAGTTCTCTGTGTGTTTCCCTGGCTCTGTGAAGGAAATCC 1008
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
DB 1009 ACTCTAGTCCCTACCTGATTTCTCAGCTTTCAGCTTGTTCACATTTGGGCAAC 1068
QY 161 ArgIleLeuProAsnLeuTyrLeuGlyCysGlnArgAspValLeuAsnLysGlnLeu 180
DB 1069 GGAATCTTCCCAATCTTATCTTGCGCCAGCAGAGATGCTTCAACAAGAGACTCATG 1128
QY 181 GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyrThrCysProLysProAspPhe 200
DB 1129 CAGCAGAAATGGGATTTGGTTATGTGTTAAATCCAGCAATACCTGTCCAAAGCTGACTT 1188
QY 201 IleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGluLysIleLeu 220
DB 1189 ATCCCCGAGTCTCATTTCTCGTGGCTGTGAATGACAGCTTTGTGAGAAATTTTG 1248
QY 221 ProThrLeuAspLysSerValAspPheIleGluLysAlaLysAlaSerAsnGlyCysVal 240
DB 1249 CCGAGTGTGCAAAATCAGTGAATTTCAATGAGAAAGCAAAAGCTTCAATGATGTGTT 1308
QY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
DB 1309 CTATGTGACCTGTTTAACTGGGATCTCCCGCTCCGCCACATCGCTATCGCTACATCATG 1368
QY 261 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLysArgProThr 280
DB 1369 AAGGAGTGAAGCATGCTTTTGAATGAAGCTTACAGATTTTGAAAGAAAAAGACTACT 1428
QY 281 IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysLysIleLysAsn 300
DB 1429 ATATCTCCAAACCTTCAATTTCTGGGCCAACTCTGGACTATGAGAAAGATTAAAC 1488
QY 301 GlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuHisLeuGluLysProAsn 320
DB 1489 CAGACTGAGATCAGGGCCAAAGACAACTCAAGCTGTGCTGCACTGGAGAAAGCCAAAT 1548

QY 321 GluProValProAlaValSerGluGlyGlnLysSerGluThrProLeuSerProPro 340
DB 1549 GAACCTATCCCTGTGTCTAGAGAGGAGAGCAAGAAAAAGCAGAGCCCTCAGTCCACCC 1608
QY 341 CysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisProAlaSerVal 360
DB 1609 TGTGCCACTCTGTACTCAGAGGCGAGAGCAAAAGGCCCTGCATCCCGCAGGCTG 1668
QY 361 ProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAlaLeu 380
DB 1669 CCCAGCTGGCCAGCGCGCAGCCGCTGTTAGAGGACGCCGCTGTACAGGCGCTC 1728
QY 381 SerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLysArgSerPhe 400
DB 1729 AGTGGCTGCACTGTCCCGACAGAGCTGGAAGACAGCAATAGCTCAAGCGTTCTTC 1788
QY 401 SerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPhe 420
DB 1789 TCTCTGATATCAAAATCAGTTTATATTCAGCAGCATGSCAGCATCTTACATGGCTTC 1848
QY 421 SerSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAspGlyThrAsn 440
DB 1849 TCCTCATCAGAAAGATGCTTGGAAATCTCAAACTTCCACTACTCTGATGGAGCAAC 1908
QY 441 LysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSerPro 460
DB 1909 AAGCTATCCAGATTCCTCCCTGTTCAAGAACTATCCGAGACAGCTCCGAAACCATCT 1968
QY 461 AspLysGlnGluAlaSerIleProLysLeuGlnThrAlaArgProSerAspSerGln 480
DB 1969 GATTAAGAGAGAAACCCAGCATCCCAAGAAAGCTCAACGCGCAGGCTTCAGACACCAG 2028
QY 481 SerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500
DB 2029 AGCAGAGATGATTCGGTGGCAGAACCGAGAGGCGACCGCCCAAGAGTCCCTTTTA 2088
QY 501 SerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheGly 520
DB 2089 TCTCCATGCTATGAAAGTGGAGCGTGGAGAAATTAACAACACGACTTCCCTTTCGGC 2148
QY 521 LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLysGlyTyrPhe 540
DB 2149 CTTTCCACCGCAGCAGACACTCAGAAATCTGTGGCTGGGCTGTAAAGGCTGCGAC 2208
QY 541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPheAla 560
DB 2209 TCGGATATCTTGGCCCCCAGACCTTACCTTCCCTGACAGCAGCTGTGATTTGGC 2268
QY 561 ThrGlnSerSerHisPheTyrSerAlaSerAlaIleTyrGlySerAlaSerTyrSer 580
DB 2269 ACAGAGTCTCAGACTTACTCTGCTCAGCATCTTACGAGGCGAGTCCGATTACTCT 2328
QY 581 AlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgAspArg 600
DB 2329 GCTTACAGCTGCAGCGCAGCTGCCACTTGCAGAGCAAAAGTCAATTTCTGTGGCAGGCG 2388
QY 601 GlnLysProSerAspArgAlaAspSerArgArgSerTyrHisGlnGlnSerProPheGln 620
DB 2389 CAGAACCAAGTACAGACTGACTCGCGCGAGCTGGCAATGAAGAGCCCTTTGAA 2448
QY 621 LysGlnPheLysArgArgSerCysGlnMetGluPheGlyGlnSerIleMetSerGluAsn 640
DB 2449 AAGCAGTTTAAACGAGAAAGCTGCCAAATGGAATTTGGAGAGCATCATGTCAAGAGAAC 2508
QY 641 ArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetGlu 660
DB 2509 AGGTCAAGGAAAGAGCTGGGAGAAAGTGGCAATGCTTAAGCTTTTTCGGCGAGCATGGAA 2568
QY 661 IleIleGluValSer 665
DB 2569 ATCATTAAGTGTCTCC 2583

Accession	Gene	Protein	Length	Score	Similarity	Local Similarity	Query Match	DB
ABV26923	standard; CDNA; 5145 BP.							
ABV26923	16-SEP-2002 (first entry)							
Human prostate expression marker CDNA 26914.								
Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker; pharmacogenomic marker; gene; ss.								
Homo sapiens.								
MO200160860-A2.								
23-AUG-2001.								
20-FEB-2001; 2001MO-US005171.								
17-FEB-2000; 2000US-0183319P.								
16-MAR-2000; 2000US-0189862P.								
25-MAY-2000; 2000US-0207454P.								
09-JUN-2000; 2000US-0211314P.								
18-JUL-2000; 2000US-0219007P.								
13-DEC-2000; 2000US-0255281P.								
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.								
Schlegel R, Endege WO, Monahan JE;								
WPI; 2001-662795/76.								
Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.								
Claim 1; Page 5449-5450; 11750pp; English.								
The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodynamic or pharmacogenomic marker								
Sequence 5145 BP; 1408 A; 1135 C; 1253 G; 1346 T; 0 U; 3 Other;								
Alignment Scores:								
Pred. No.: 0	Length: 5145							
Score: 3406.00	Matches: 663							
Percent Similarity: 99.85%	Conservative: 1							
Best Local Similarity: 99.70%	Mismatches: 1							
Query Match: 99.65%	Indels: 0							
DB: 1	Gaps: 0							
US-10-029-345A-109 (1-665) x ABV26923 (1-5145)								
1	1							
589	589							
21	21							
649	649							
708	708							

Db 1789 TCTCGAATATCAAAATCAGTTTCATATTCAGCAGATGCGACATCTTATCATGCTTC 1848
QY 421 SerSerSerGluAspAlaLeuGluTyrTyrLeuProSerThrThrLeuAspGlyThrAsn 440
Db 1849 TCTCATCAAGAAAGATCTTGGAAATCTCAAAACCTTCCACTACTCTGGATGGACCAAC 1908
QY 441 LysLeuGlyGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSerPro 460
Db 1909 AAGCTATGCGAGTCTCTCCCTGCTTCAAGAACTATCGAGACAGACTCCGAAACAGTCTCT 1968
QY 461 AspLysGluGlnAlaSerLeuProLysLysLeuGlnThrAlaArgProSerAspSerGln 480
Db 1969 GATTAAGAGAAAGCAAGCATCCCAAGAAAGCTGACAGCCGACCTTTCAGACAGCCAG 2028
QY 481 SerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500
Db 2029 AGCAAGCAATTCATTCCTGCTGAAACCAAGACAGACTGGACCCGCAAGGTCCTTTTA 2088
QY 501 SerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheGly 520
Db 2089 TCTCCACTGATCATGAAGTGGAGCGTGGAGGACAAATTACACACAGCTTCTTTTGGC 2148
QY 521 LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLysGlyTyrPhe 540
Db 2149 CTTTCACCAAGCAGACAGACCTCAAGAGTCTGCTGGCTGGGCTTAAGGGCTGGCAC 2208
QY 541 SerAspLeuLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPheAla 560
Db 2209 TCGGATATCTTGGCCCCCAAGCTCTTACCTTCCCTGACCAAGACGCTGGTATTTTCC 2268
QY 561 ThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyLysSerLysSerTyrSer 580
Db 2269 ACAGAGTCTCTACACTTACTCTGCTCAGCACTCAAGGAGGAGGAGGAGGAGGAGTACTCT 2328
QY 581 AlaTyrSerCysSerGlnLeuProThrCysGlyValAspGlnValTyrSerValArgArgArg 600
Db 2329 GCTTACAGCTGACGACCTGCTCCACTTGCAGAGCAAAAGCTTTCTGTCGAGGCGG 2388
QY 601 GlnLysProSerAspArgAlaAspSerArgArgSerTyrPheGlnGluLysSerProPheGln 620
Db 2389 CAGAAAGCAAGTGAAGAGCTGACTCGCGGAGCTGCAATGAAGAGGCCCTTTGAA 2448
QY 621 LysGlnPheLysArgArgSerCysGlnMetGluPheGlyLysSerLysSerGluAsn 640
Db 2449 AAGCAGTTTAAACGACAGAACTGCCAAATGGAATTGAGAGAGCATCATCTCAGAGAAC 2508
QY 641 ArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetGlu 660
Db 2509 AGGTACCGGAAAGAGCTGGGAAAGTGGGAGTCACTAGCTTTTCGGGACAGCATGAA 2568
QY 661 IleIleGluValSer 665
Db 2569 ATCATTTAGGTCTCC 2583

RESULT 6
ABV27135
ID ABV27135 standard; cDNA; 5145 BP.
XX ABV27135;
AC
XX
XX 16-SEP-2002 (first entry)
DT
XX
XX Human prostate expression marker cDNA 27126.
DE
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
OS
XX W0200160860-A2.
PN
XX 23-AUG-2001.

XX
PF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JR;
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 5502-5503; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 5145 BP; 1408 A; 1135 C; 1253 G; 1346 T; 0 U; 3 Other;
Alignment Scores:
Pred. No.: 0 Length: 5145
Score: 3406.00 Matches: 663
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.65% Indels: 0
DB: 1 Gaps: 0
US-10-029-345A-109 (1-665) x ABV27135 (1-5145)
QY 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGlu 20
Db 589 ATGGCCCATGAGATGATTGGAACCTCAAAATTGTTACTGAAGAGTGGCTCGCTGGAA 648
QY 21 SerGlyThrGluLysValLeuLeuIleAspSerArgProPheValGluLysThrPheSer 40
Db 649 AGTGAACGAAAGAGAGTGGCTGCTAATTGATTAACCGGCACTTTGTGAATTAACAATCATCC 708
QY 41 HisIleLeuGlnAlaIleAsnIleAsnCysSerLysLeuMetLysArgArgLeuGln 60
Db 709 CACATTTTGAAGCCATTATATCAACTGCTCCAGACTTATGAAGAAAGTTTGAACAG 768
QY 61 AspLysValLeuIleThrGluLeuIleGlnHisSerAlaLysHisLysValAspIleAsp 80
Db 769 GACAAAGTGTATTATTAACAGAGCTCATCCAGCAATTACGCAAAACATTAAGTTGACATTGAT 828
QY 81 CysSerGlnLysValValValTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
Db 829 TGCAGTCAGAAAGGTGTATTTACATCAAAAGCTCCCAAGATGTGCTCTCTCTTCA 888
QY 101 AspCysPheLeuThrValLeuLeuGlyLysLeuGluLysSerPheAsnSerValHisLeu 120
Db 889 GACTGTTTCTCAGCTGATCTCTGGGTAACTGGAAGAGAGCTTCAACTCTTTCACCTG 948
QY 121 LeuAlaGlyLysPheAlaGluPheSerArgCysPheProGlyLeuCysGluGlyLysSer 140

Db 949 CTTCAGAGTGGTTTGCTGAGTCTCTCGTTGTTTCCCTGCGCTCTGAGAGGAAATCC 1008
 Qy 141 ThrLeuValProThrCysIIleSerGlnProCysLeuProValAlaIleuIIleGlyProThr 160
 Db 1009 AGCTACATCCCTACCTGCAATTTCTCAGCCTTGCTTACTGTGCGCAACATTTGGCCAAACC 1068
 Qy 161 ArgIIleLeuProAsnLeuTyrLeuGlyCysGlnArgAspValLeuAsnIleGlyLeuIle 180
 Db 1069 CGAATTCCTCCCAATCTTTACTTTGGCTGCGCAGGAGAAATGCTCTCAACAAAGAGCTGATG 1128
 Qy 181 GluGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyrThrCysProIleProAspPhe 200
 Db 1129 CACAGAGATGGATGGTTATGTGTTAAATGCCAGCAATACCTGTCCAAAGCCTGACTTT 1188
 Qy 201 ILProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlyIleu 220
 Db 1189 ATCCCCAGAGTCAATTCCTGCGTGTGCGTGAATACAGACTTGTGTGAAATTTTG 1248
 Qy 221 ProTrpLeuAspIlePheValAspPheIIleGlyIleValAlaIleAsnGlyCysVal 240
 Db 1249 CCGTGGTTGGACAATCAGTAGATTTCATTGAGAAACAAAGCTCCATGGATGTT 1308
 Qy 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
 Db 1309 CTAGTGCACTGTTAGCTGGGATCTCCGCTCGCCACATCGCTATCGCTACATCATG 1368
 Qy 261 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValIleGlyIleValAspProThr 280
 Db 1369 AAGAGGTGAGACATGCTTTAGTAGAAGCTTACAGATTGTGAAAGAAAGAAAGCCTACT 1428
 Qy 281 ILleSerProAsnPheAsnPheLeuGlyIleLeuLeuAspTyrGlyIleValAsn 300
 Db 1429 ATATCTCCAAACTTCAATTTTCTGGCCAACTCCTGACATATGAGAAAGATTAGAAC 1488
 Qy 301 GlnThrGlyAlaSerGlyProIleSerLeuLeuIleLeuIleLeuGlyIleValProAsn 320
 Db 1489 CAGACTGAGACATCAGGCGCAAGAGCAAACTCAAGCTGTGCGACCTGGAGAGCCAAAT 1548
 Qy 321 GluProValProAlaValIleSerGluGlyIleGlyIleSerGluThrProLeuSerProPro 340
 Db 1549 GAACCTGCTCCTCTGCTCAGAGGCTGACAGAAAGGCAAGAGCCCTCAGTCCAGCC 1608
 Qy 341 CysAlaAspSerAlaThrSerGluAlaAlaGlyIleGlnArgProValHisProAlaSerVal 360
 Db 1609 TGTGCCGACTCTCTACTCAGAGGCGACGACGACAAAGGCCCTGCTATCCCGCAGGCTG 1668
 Qy 361 ProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAlaLeu 380
 Db 1669 CCCAGCGTCCAGCGTGCAGCGCTGCTGTAGAGGACGCCGCTGTACAGGCGCTC 1728
 Qy 381 SerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnIleLeuIleValSerPhe 400
 Db 1729 AGTGGGCTGACCTGTCCGAGACAGGCTGAAAGACGAAATAGCTCAAGCGTTCCTTC 1788
 Qy 401 SerLeuAspIleLeuSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPhe 420
 Db 1789 TCTCTGATATCAATAGATTTCATATTCAGCCAGCATGCGACATCTTCAATGCTTC 1848
 Qy 421 SerSerSerGluAspAlaLeuGluTyrTyrIlePheProSerThrThrLeuAspGlyThrAsn 440
 Db 1849 TCCTTCATCAAGAAATGCTTTGAAATACTCAAACTTCCACTCTGATGGAGACCAAC 1908
 Qy 441 LysLeuGluGlnPheSerProValGlnGluLeuSerGluGlnIleThrProGluThrSerPro 460
 Db 1909 AAGCTATGCGAGTCTCCCTGTTCAAGAACTATCGAGAGAGACTCCCGAAACAGGCTC 1968
 Qy 461 AspLysGluGluAlaSerIleProIleValLeuGlnThrAlaArgProSerAspSerGln 480
 Db 1969 GATAGAGAGAGAGCAGACATCCCAAGAACTGCAAGCCCGCAGGCTTTAGACAGCCAG 2028
 Qy 481 SerIleValArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500
 Db 2029 AGCAAGCGATTGATTCGTCAGAACAGAGCAGTGGCAGCCCGCAGAGGTCCCTTTTA 2088

Qy 501 SerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheGly 520
 Db 2089 TCTCCATGATGAAAGTGGAGCTGAGAGACAAATTACCAACCGACTTCTTTCCGCG 2148
 Qy 521 LeuSerThrSerGlnIleLeuThrIleValSerAlaGlyLeuGlyLeuIleValSerIle 540
 Db 2149 CTTTCACAGCAGCAGAGCAGCCTCACAGATGTGTGTGGCTGGGCTTAAAGGCTGGCAC 2208
 Qy 541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPheAla 560
 Db 2209 TCGATATCTTGGCCCCCAGACCTTACCCCTTCCCTGACAGCAGCTGTGATTTTGCC 2268
 Qy 561 ThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyIleSerAlaSerTyrSer 580
 Db 2269 ACAGAGTCTTCACACTTCTTACTGCTTCAACCATTTACGAGGCGATGCGCAATTACTCT 2328
 Qy 581 AlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArgArg 600
 Db 2329 GCTTACAGCTGACAGCAGCTGCCACTTGGCGAGACCAAGTCTATTCTGTGCGCAGCGG 2388
 Qy 601 GlnIleProSerAspArgAlaAspSerArgArgSerTyrHisGlyIleGluIleSerProPheGlu 620
 Db 2389 CAGAACCAAGTGAAGAGCTGACTGCGCGCGAGCTGGCATGAAAGAGACCCCTTTGAA 2448
 Qy 621 LysGlnPheLysArgArgSerCysGlnMetGluPheGlyIleSerIleMetSerGluAsn 640
 Db 2449 AAGCATTTTAAACGCAAGAGCTGCCAAATGGAATTTGGAGAGCATCATGTACAGAAC 2508
 Qy 641 ArgSerArgGluGluLeuGlyIleValGlySerGlnSerSerPheSerGlySerMetGlu 660
 Db 2509 AGGTCAAGGGAAGAGCTGGGGAAGTGGGAGTCAAGTCACTTTCGGGCAACATGGA 2568
 Qy 661 IleIleGluValSer 665
 Db 2569 ATCATTTAGAGTCTCC 2583

Db 2569 ATCATTTAGAGTCTCC 2583

RESULT 7
 ABV28657 standard; cDNA; 5145 BP.
 ABV28657;
 AC 16-SEP-2002 (first entry)
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 28648.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynanamic marker;
 KM pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001MO-US005171.
 XX
 PR 17-FEB-2000; 2000US-018319P.
 PR 16-MAR-2000; 2000US-0189862P.
 PR 09-MAY-2000; 2000US-0207454P.
 PR 09-JUN-2000; 2000US-0211314P.
 PR 18-JUL-2000; 2000US-0219007P.
 PR 13-DEC-2000; 2000US-0255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JB;
 XX
 DR WPI, 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful

for detecting presence of prostate cancer, stage of prostate cancer.

PS Claim 1; Page 6009-6010; 11750pp; English.

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV6221) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) (I) is also useful as a pharmacodynamic or pharmacogenomic marker

SQ Sequence 5145 BP; 1408 A; 1135 C; 1253 G; 1346 T; 0 U; 3 Other;

Alignment Scores:

Pred. No.:	0	Length:	5145
Score:	3406.00	Matches:	663
Percent Similarity:	99.85	Conservative:	1
Best Local Similarity:	99.70%	Mismatches:	1
Query Match:	99.65%	Indels:	0
DB:	1	Gaps:	0

US-10-029-345A-109 (1-665) x ABV28657 (1-5145)

QY	1	MEALHHSGLMVECTLEGIYThrGlnIleValThrGlnArgLeuValAlaLeuLeuGln	20
Db	589	ATGGCCCAAGAGATGATGGAACTCAAAATTGTACTAGAGGTTGGTGGCTCTGGCGAA	648
QY	21	SeSGlyThrGlnLysValLeuLeuIleAspSerArgProPheValGlnTyraenThrSer	40
Db	649	AGTGGACACGGAAAAATGGCTGCTAAATTATGACCGCGCATTTTGGTAATCAATATCATCC	708
QY	41	HisIleLeuGlnValIleAsnIleAsnCyseSerLysLeuLeuTyrAspGlyLeuGln	60
Db	709	CACATTTTGGAGCCATTATATATCAACTGCTCCAAAGCTTATGAAAGCAAGTTTGCACACG	768
QY	61	AspLysValLeuIleIleThrGlnLeuIleGlnHisSerAlaLysHisLysValAspIleAsp	80
Db	769	GACAAAGATGTAAATTACAGAGCTCATCCAGCATTCACAGAAACATTAAGTTGACATTGAT	828
QY	81	CySeSerGlnLysValValValTyrAspLysIleSerGlnAspValAlaSerIleuSerSer	100
Db	829	TGCAGTCACAAAGTTGTAGTTAGATACAAAGCTCCCAAGATGTGGCTCTCTCTTCA	888
QY	101	AspCySePheLeuThrValLeuLeuGlnLysIleLeuLysSerPheAsnSerValHisLeu	120
Db	889	GACTGTTTTCTCACTGACTGACTTGTGGGTAACATGGAGAAAGCTTCAACTGTTCACCTG	948
QY	121	LeuValGlyGlyPheAlaGlnPheSerArgCySePheProGlyLeuCyGlnGlyLysSer	140
Db	949	CTTGCAGAGGTGGTTCGTGAGATTCCTGTGTTTCTCTGGCCCTGTGTGAAGGAAATCC	1008
QY	141	ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr	160
Db	1009	ACTCTAGTCCCTACTGCACTTTCACAGCTTGCTTACTGCTGTGCACAACTGGGCACACC	1068
QY	161	ArgIleLeuProAsnLeuTyrLeuGlnLysGlnIleArgAspValLeuAsnLysGlnLeuIle	180
Db	1069	CGAAATTTTCCAAATCTTATATCTGGGCGCCAGGAGAAATGTCTTCAACAAGAGCTGATG	1128
QY	181	GlnGlnAsnGlyIleGlyTyrValIleAsnAlaSerGlyThrCysAspProLysProAspPhe	200
Db	1129	CAGCAGAAATGGGATTGGTTATCTGTTAATGCCACGAACTACTCTGTCCAAAGCTGACTTT	1188
QY	201	IleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGlnLysIleLeu	220
Db	1189	ATCCCCGAGTCCATTTCTCTCGGTGCTGTGTGAATACACGCTTTTGTATGAAAATTTTGG	1248

QY	222	ProTPrleuAspIysSerValAspPheIleGIuIysAlaIysAlaSerAsnGIyCySerVal	240
Db	1249	CCGTGGTGGACAAATACGTAGATTTCATTGAGAAAGCAAAAGCCCTCAAGAGAGTGT	1308
QY	241	IeuValIhISCyValIeuAGIyIleSerIySerSerAlaThrIleAlaIleAlaIyTrIleMet	260
Db	1309	CTAGTGACACTGTTAGTGGGATCTCCGGCTCCGCACCATTCGATAGCTTACATCAT	1366
QY	261	LybAlaGMeIaSPMeSerIleuAspGIuAlaTyraGpheValIySGIuIyAspProThr	280
Db	1369	AAGAGAAATGACATCTCTTGTAGTAAACCTTACAGATTGTGAAAGAAAAAGACCTTCT	1428
QY	281	IleSerProAsnPhenPheAsnIleuGIyGIuIleuIeuAspIyryGIuIyIyIleIyAsn	300
Db	1429	ATATCTCCAAACTTCATTTTTCTGGGCCAACTCTCGACATATGAGAGAAATTTAAGAC	1488
QY	301	GIuThrGIyAlaISerGIyProlIySerIyIleuIyIleuIhISleuGIuIyAspAsn	320
Db	1489	CAGACTGAGAGATCAGGGCCAAAGAGCAAACTCAAGCTGCGACCTTGAGAAACCAAT	1548
QY	321	GIuProValProAlaValISerGIuGIyGIuIyIySerGIuThrProIeuSerPro	340
Db	1549	GAACTGTCCCTGCTGTCTTCAGAGGGTGGACGAAAGCCGAGAGCCCTTAGTCCACC	1608
QY	341	CysAlaAspSerAlaIhISerGIuAlaAlaAGIyGIuIyIyIhISProAlaSerVal	360
Db	1609	TGTGCGCACTCTGCTACCTCAGAGGACAGACAGAAAGCCGTCATCCCGCAGCGTG	1668
QY	361	ProSerValProSerValGIuIyProSerIleuIeuIuAspSerProIeuValGIuAlaIeu	380
Db	1669	CCAGCCGGCCACAGTGCAGCCCGTCTGTTAAGACAGCCCGCTGGTACAGCGCTC	1728
QY	381	SerGIyIeuIhISleuSerAlaAspArgIeuIuAspSerAsnIyIleuIyAspSerPhe	400
Db	1729	AGTGGGCTGCACCTGTCCGACAGAGAGCTGSAACAGCAATTAAGCTTAAGCTTCTTC	1788
QY	401	SerIeuAspIleIyISerValSerTyISerAlaSerMeAlaIleSerIeuIhISGIyPhe	420
Db	1789	TCTCTGAGATACAAATCAGTTTCATTTACGCCAGCATGGAGATCCTTAACATGGCTTC	1848
QY	421	SerSerSerGIuAspAlaIeuGIuTyTyIyIyAspSerThrThrIleuAspGIyThraSn	440
Db	1849	TCCCTCATCAGAAAGTCTTGTGAAATACTCAAACTTCCACTACTCTGGATGGACCAAC	1908
QY	441	IyISeuCysGIuIhISerProValGIuIyIeuSerGIuIuThrProGIuThrSerPro	460
Db	1909	AAGCTATGCCAGTCTCTCCCTGTTACAGAACTATCGAGACAGACTCCGAAACCAAGCTT	1968
QY	461	AspIySGIuGIuIaSerIleProlIyIyIeuGIuIhIaIyAspProSerAspSerGIu	480
Db	1969	GATAGAGAGAGACACACATCCCAAGAAACCTGAGCCGCCAGCCCTTACAGACAGCAG	2028
QY	481	SerIyAspIyIeuIhISerValArgThISerSerSerGIyThraIAGIuIySerIleu	500
Db	2029	AGCAAGCATTTGCACTTCGTCAAGACCAAGACAGCAGTGGACCCGCCAGAGTCCCTTTTA	2088
QY	501	SerProIeuIhISarGSerGIyISerValGIuAspAsnTyThIShrSerPheIeuPheGIy	520
Db	2089	TCTCCACTGATCGAAATGGAGACGTGGAGAGAAATTAACACACAGCTTCTTTTCGGC	2148
QY	521	IeuSerThrSerGIuIhISleuThrIyISerAlaGIyIeuGIyIeuIySGIyTPHIS	540
Db	2149	CTTTCCACCAAGCCAGACACCTCAAGAAGTCTGTGGCTGGGCTTTAAGGCTGGCAC	2208
QY	541	SerAspIleIeuAlaProGIuThrISerThrProSerIeuThrSerSerTPyIyPheAla	560
Db	2209	TCCGATATCTTGGCCCCCCAGACCTCTCAACCTTCCCTGACACAGCTGTGATTTTGGCC	2268
QY	561	ThnGIuISerSerIhISpHeTyISerAlaISerAlaIleIyGIyIyIySerAlaISerTySer	580
Db	2269	ACGAGAGTCTTCAACATTTCACTGTGCTCAGCCATCTACGAGAGCGAGTGCAGATTACTCT	2328
QY	581	AlaTyISerCySerGIuIeuProThrCySGIyAspGIuValTyISerValIAGTAgArg	600

Db 2329 GCCTACAGCTGACGCCAGCTGCCCCACTTGCGGAGACCAAGTATCTGTGCCAGCGG 2388
QY 601 GlnlyProSerSerppaaglaaapSerArgArgSerTrpHlaGluSerProPheGlu 620
Db 2389 CAAAGCCAAAGTACAGAGCTGACTCCGCGGAGCTGCGATAGAAAGACCCCTTTGAA 2448
QY 621 LysGlnPheIysArgArgSerCysGlnMetGluPheGluYgluSerIleMetSerGluAsn 640
Db 2449 AACGAGTTTAAACGCAGAACCTGCCAATGGAATTTGAGAGAGCATCATGTCAAGAAC 2508
QY 641 ArgSerArgGluGluLeuGlyIlyValGlySerGlnSerSerPheSerGlySerMetGlu 660
Db 2509 AGGTCAAGGAGAAAGCTGGGAAAGTGGCAGTCAAGTCTTTTGGGCGACGATGAA 2568
QY 661 IleIleGluValSer 665
Db 2569 ATCATTTGAGGTCTCC 2583
RESULT 8
ABV22827
ID ABV22827 standard; cDNA; 5145 BP.
XX
AC ABV22827;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 22818.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KM pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN MO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001MO-US005171.
XX
PR 17-FEB-2000; 2000US-018319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI, 2001-662795/76.
XX
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 4033-4034; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the efficacy
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
XX Sequence 5145 BP; 1408 A; 1135 C; 1253 G; 1346 T; 0 U; 3 Other;

Alignment Scores:
Pred. No.: 0 Length: 5145
Score: 3406.00 Matches: 663
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.65% Indels: 0
Gaps: 0
US-10-029-345A-109 (1-665) x ABV22827 (1-5145)
QY 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGlu 20
Db 589 ATGGCCCATGAGATGATTTGGAACCTCAAAATTGTTACTGAGAGGTTGGCTCTGCTGAA 648
QY 21 SerGlyThrGluIlyValLeuLeuIleAspSerArgProPheValGluTyrAantThrSer 40
Db 649 AGTGAACCGAAMAAAGTGTGCTGAATTTGATAGCCGCCCATTTTGTGAAATTAACAATCAC 708
QY 41 HisIleLeuGluValAlaIleAsnIleAsnCysSerIlyLeuMetIysArgArgLeuGln 60
Db 709 CACATTTTGGAGCCATTATTAATCACTGCTCCAAAGCTTATGAAAGGAGTTGCCAACAG 768
QY 61 AspIlyValLeuIleThrGluLeuIleGlnHisSerAlaIlyHisIlyValAspIleAsp 80
Db 769 GACAAAGTGTATTAACAAGCTCATCCAGCATTCAGCGAAACATAAGTTGACATTGAT 828
QY 81 CysSerGlnIlyValValIlyValIlyAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
Db 829 TGCAGTCAGAAAGTGTAGTTTACGATCAAAAGCTCCCAAGATTTGCTCTCTCTTCA 888
QY 101 AspCysPheLeuThrValLeuLeuGlyIlyValLeuGluIlySerPheAsnValHisLeu 120
Db 889 GACTGTTTCTCACTGTTACTTCTGGTTAACTGGAAGAGCTTCAACTCTGTTCACTG 948
QY 121 LeuAlaGlyIlyPheAlaGluPheSerArgCysPheProGlyLeuGlyIlySer 140
Db 949 CTTCGAGAGTGGGTTTCTGAGTTCTCTCGTTGTTTCCCTGCGCTCTGTGAAGAAATCC 1008
QY 141 ThrLeuValProThrCysAlleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
Db 1009 ACTCTAGTCTCTCACTGCAATTTCTCAAGCTTCTGCTTCACTGTTGCCAACATTTGGCCAA 1068
QY 161 ArgIleLeuProAsnLeuIlyLeuGlyCysGlnArgAspValLeuAsnIlyGluLeu 180
Db 1069 CGAATTTCTCCAAATTTTATCTTGCTGCGCACAGAGTCTTCAACAAGAGCTGATG 1128
QY 181 GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyrThrCysProIlyProAspPhe 200
Db 1129 CAGCAGATGAGATTTGTTATGTTTAATGCCAGCAATACCTGCCAAAGCTGACTTT 1188
QY 201 IleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluIlyValLeu 220
Db 1189 ATCCCGAGTCTATTTCTGCGCTGTGCTGTGAAGACAGCTTTTGTGGAATAATTTTG 1248
QY 221 ProThrLeuAspIlySerValAspPheIleGluValAlaIlyValAsnIlyCysVal 240
Db 1249 CCGTGTGTGACAAATCAGTATTCATTTGAAAGCAAAACCTCCAAATGATGTT 1308
QY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
Db 1309 CTAGTGCACGTTTACTGCTGGAGTCTCCGCTCGCCACACATGCTTACGCTTACATCATG 1368
QY 261 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValIlyGluIlyValAspProThr 280
Db 1369 AAGAGGATGACATGCTTTAGTGAAGCTTACAGATTTGTGMAAAMAAACCTACTACT 1428
QY 281 IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluIlyValIlyAsn 300
Db 1429 ATATCTCCAAACTTCAATTTTCTGGCCAACTCTTGACATATGAGAAAGATTTAAGAAC 1488
QY 301 GlnThrGlyAlaSerGlyProIlySerIlyLeuIlyLeuLeuHisLeuGluIlyProAsn 320

Db 1489 CAGACTGGAGCATCAGGGCCAAAGACAACTCAAGCTGCTGACCTGGAGAGCCAAAT 1548
Qy 321 GIUProValProAlaValSerGluGlyGlnIleuSerGluThrProIleuSerProPro 340
Db 1549 GAACCTGTCTCTGTCTCTCAGAGGTTGACAGAAAAGGAGAACGCCCCCTCAGTCCACCC 1608
Qy 341 CysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisProAlaSerVal 360
Db 1609 TGTGGCCAGTCTGTACTACCTCAGAGGCGAGAGCAAAAGGCCGCTGATCCGCCAGCGTG 1668
Qy 361 ProSerValProSerValGlnProSerIleuGluuAspSerProIleuValGlnAlaIleu 380
Db 1669 CCCAGCTGCCAGGCTGACGCGTGTGTTAGAGAGACGCCCGCTGTACAGGCGTCTC 1728
Qy 381 SerGlyIleuHisIleuSerAlaAspArgIleuGluAspSerAlaIleuValArgSerPhe 400
Db 1729 AGTGGGCTGTGCACCTGTCCGACAGAGGCTGAGAAACAGAAATACCTCAAGCTTCTTC 1788
Qy 401 SerIleuAspIleuValSerValSerValSerAlaSerMetAlaAlaSerIleuHisGlyPhe 420
Db 1789 TCTCTGGATATCAAAATCAGTTTCATATTCAGCCAGCATAGGCGATCCTTACATGGCTTC 1848
Qy 421 SerSerSerGluAspAlaIleuGlnIleuValIleuValProSerThrThrIleuAspGlyThrAsn 440
Db 1849 TCTCATCAGAAAGATGCTTTGGAAATACAAACCTTCACACTACTGTGATGGAGCCAC 1908
Qy 441 LysIleuCysGlnIleuSerProValGlnIleuSerGluGlnThrProGluThrSerPro 460
Db 1909 AAGCATATGCAGATCTCTCCCTGTGTGAGAACTATGAGAGAGACTCCCGAAACCACTCT 1968
Qy 461 AspLysGluGluAlaSerIleuValIleuValIleuGlnIleuValIleuValProSerAspSerGln 480
Db 1969 GATTAAGAGAGAAAGCAGATCCCAAGAGCTGCAGACCGCCAGGCTTCAGACAGCCAG 2028
Qy 481 SerLysAspGluHisSerValArgThrSerSerSerSerGlyThrAlaGlnArgSerIleu 500
Db 2029 AGCAAGCATTTGCATTCGGTCAAGAACAGACAGCATGSCACCGCCAGAGTCCCTTTTA 2088
Qy 501 SerProIleuHisArgSerGlySerValGlnuAspAntyRhiArgSerPheIleuPheGly 520
Db 2089 TCTCCACTGCATTCGAAGTGGAGCGTGGAGAGCAATATCCACACCAAGCTTCTTTGGGC 2148
Qy 521 LeuSerThrSerGlnHisIleuThrIleuSerAlaGlyIleuGlyIleuValGlyTyrHis 540
Db 2149 CTTTCACACAGCAGACACCTCAGCAAGTCTGTGCTGGCTTAAAGGCTGCAC 2208
Qy 541 SerAspIleuAlaProGlnThrSerThrProSerIleuThrSerSerTyrPheAla 560
Db 2209 TCGGATATCTGGCCCCCAGACCTTACCCCTTCCGACCAAGCTGTGATTTTGCC 2268
Qy 561 ThrGluSerSerHisPheTyrSerAlaSerAlaIleuValGlyIleuValSerTyrSer 580
Db 2269 ACAGAGTCTCACTTCTACTGCTGCTCAGCCATCTACGAGGCAAGGCCAGATTACTCT 2328
Qy 581 AlaTyrSerCysSerGlnIleuProThrCysGlyAspGlnValTyrSerValArgArgArg 600
Db 2329 GCTTACAGCTCAGCAGCTGCCCACTTGGGAGAACCAAGCTATCTGTGCGCAGGCGG 2388
Qy 601 GlnIleuProSerAspArgAlaAspSerArgArgSerTyrHisGlnIleuSerProPheGlu 620
Db 2389 CAGAAAGCCAAAGTGAAGAGCTGACTCGGCGGAGGCTGGCATGAAGAGACCCCTTTGAA 2448
Qy 621 LysGlnIleuValArgArgSerCysGlnMetGluPheGlyIleuSerIleuMetSerGluAsn 640
Db 2449 AAGGAGTTTAAACCAAGAGCTGCCAAATGGAATTTGAGAGGACATGTCAGAGAAC 2508
Qy 641 ArgSerArgGluGluIleuValGlyValGlySerGlnSerSerPheSerGlySerMetGlu 660
Db 2509 AGGTCACGGAGAGAGCTGGGAAAGTGGCACTGATGCTTGTGGGAGAGCATGAA 2568
Qy 661 IleIleGluValSer 665
Db 2569 ATCATGAGGCTCC 2583

RESULT 9
ABV26934
ID ABV26934 standard; cDNA: 5145 BP.
XX
AC ABV26934;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 26925.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
RW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN W0200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189662P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PI Schlegel R, Endege WO, Monahan JE;
XX
XX WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous etate of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 5453-5454; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (1) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (1) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 5145 BP; 1408 A; 1135 C; 1253 G; 1346 T; 0 U; 3 Other;
XX
Alignment Scores:
Pred. No.: 0 Length: 5145
Score: 3406.00 Matches: 663
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.65% Indels: 0
DB: 1 Gaps: 0
US-10-029-345A-109 (1-665) x ABV26934 (1-5145)
Qy 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaIleuLeuGlu 20
Db 589 ATGGCCCATGAGATGATTGGAATCAAAATTTTACTGAGAGGTTGTGCTCTGCTGGAA 648
Qy 21 SerGlyThrGluValIleuLeuIleAspSerArgProPheValGluTyrAsnThrSer 40
Db 649 AGTGAACGGAAGAAAGTGTGCTTAATTATACCGCCCAATTTGTGGAATACATACATCC 708

QY 41 HisIleuGluAlaIleAsnIleAsnCySerLysLeuMetLysArgLysGluGln 60
DB 709 CACATTTGGAAAGCATTAATCACTGCTCCAAAGCTTATGAAGCAAGGTTCCACAG 768
QY 61 AspLysValLeuIleThrGluLeuIleGlnHisSerAlaLysHisLysValAspIleAsp 80
DB 769 GACAAAGTGTAAATTACAGAGCTCATCCAGCATTCACGAAACATAAGTTGACATTGAT 828
QY 81 CysSerGlnLysValValValTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
DB 829 TGCAGTCAGAGGTTGATGTTACGATCAAGCTCCCAAGATGTGCTCTCTCTTCA 888
QY 101 AspCysPheLeuThrValLeuLeuGlyLysLeuGlnLysSerPheAsnSerValHisLeu 120
DB 889 GACGTTTTCTCACTGACTGCTTGGGTAACTGGAGAAAGACTTCACACTGTTCACTG 948
QY 121 LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuGlyGluGlyLysSer 140
DB 949 CTTCAGAGTGGGTTGCTGAGTTCTCTGTTGTTCCCTGGCTCTGTGAAGGAAATCC 1008
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
DB 1009 ACTCTAGTCCCTACCTGCAATTTCTCAGCTTGTCTTACCTGTGCAACATTTGGCCAAC 1068
QY 161 ArgIleLeuProAsnLeuTyrLeuGlyCysGlnArgAspValLeuAsnLysGluLeuIle 180
DB 1069 CGAATTTCTCCCAATCTTTATCTTGGCTGCCAGGAGATGCTCCCAACAAAGAGCTGATG 1128
QY 181 GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyrThrCysProLysProAspPhe 200
DB 1129 CAGAGAAATGGGATGGTATGTGTAAATGCCAGCAATACCTGTCCAAAGCCGACTTT 1188
QY 201 IleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGluLysIleLeu 220
DB 1189 ATCCCCAGTCTCAATTCCTGCGGTGCTCGTGAATACAGCTTTTGTGAATAATTTTG 1248
QY 221 ProThrLeuAspLysSerValAspPheIleGluLysAlaLysAlaSerAsnGlyCysVal 240
DB 1249 CCGTGTGGAGCAAAATAGTATGATTTCAATTGAAAGCAAAAGCTCCAAATGATGTGT 1308
QY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
DB 1309 CTAGTGCACTGTTAGCTGGGATCTCCGCTCCGCCCACTCGCTATCGCTACATCATG 1368
QY 261 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLysArgProThr 280
DB 1369 AAGAGATGACATGCTTTAGATGAAGCTTACGATTTGTGAAGAAAAAGACTTACT 1428
QY 281 IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysLysIleLysAsn 300
DB 1429 ATATCTCCAAATCTCAATTTTCTGGGCCAACTCTGAGCATATGAGAAAGATTAAAC 1488
QY 301 GlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLysIleGluLysProAsn 320
DB 1489 CAGACTGAGCATCAGGGCCAAAGACAACTCAAGCTGTGACCTCGAGGAAGCCAAAT 1548
QY 321 GluProValProAlaValIleSerGluGlyGlnLysSerGluThrProLeuSerProPro 340
DB 1549 GAACCTGTCTCTGCTGCTCAGAGGGTGAACAGAAAGCAAGACGCCCTCAGTCCACCC 1608
QY 341 CysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisProAlaSerVal 360
DB 1609 TGTGCCACTCTGCTACTCAGAGGACGACGAGCAAAAGGCCGTGATCCCGCAGGCTG 1668
QY 361 ProSerValProSerValGlnProSerLeuGlnLysAspSerProLeuValGlnAlaLeu 380
DB 1669 CCCAGCTGCCAGCGTGAAGCCGTGCTGTTAAGACAGACCGCGGTGATACAGGCGCTC 1728
QY 381 SerGlyLeuHisLeuSerAlaAspArgLeuGlnAspSerLysLysLysLysLysPhe 400
DB 1729 AGTGGCTGACCTGTCCGAGACAGGCTGAAAGACAGCAATATGCTCAAGCGTTCTTC 1788

QY 401 SerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPhe 420
DB: 1789 TCTCTGGATATCAAAATCAGTTTATATTCAGCCAGCATGGACATCTTACATGGCTTC 1848
QY 421 SerSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAspGlyThrAsn 440
DB 1849 TCTCATCAGAAATGCTTTGGAAATCTACAAACCTTCCATCTCTGATGGAGCAAC 1908
QY 441 LysLeuCysGlnPheSerProValGlnLysSerGluGlnThrProGlnThrSerPro 460
DB 1909 AAGCTATGCCAGTTCCTCCCTGTTCAAGAACTATCGAGAGACTCCGAAACAGCTCT 1968
QY 461 AspLysGluGlnLysSerIleProLysLysLeuGlnThrAlaArgProSerAspSerGln 480
DB 1969 GATTAAGAGAAACCGACATCCCAAGAGCTCAGACCGCCAGGCTTACAGACAGCAG 2028
QY 481 SerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeu 500
DB 2029 AGCAGCGATTCGATTCGTCAAGAACAGCAGCAGTGGCACCCGCCAGAGTCCCTTTTA 2088
QY 501 SerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheGly 520
DB 2089 TCTCACTGCATGAGTGGAGCGTGAAGACAAATTACACACAGCTTCTTTTCGGC 2148
QY 521 LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLysGlyTyrPhe 540
DB 2149 CTTTCCACCGACGACGACGACCTCAGAAATCTGCTGGCCCTTAAGGCTGGCAC 2208
QY 541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPheAla 560
DB 2209 TCGGATATCTTGGCCCCCCAGACCTTACCCCTTCCCTGACAGAGCTGTATTTTGGC 2268
QY 561 ThrGluSerSerHisPheTyrSerAlaSerAlaIleGlyGlyLysSerAlaSerTyrSer 580
DB 2269 ACGAGCTCTCAACACTTACTGCTGCTCAGCCATCTACGAGACGAGTGCAGTTACTCT 2328
QY 581 AlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArgArg 600
DB 2329 GCCTACAGCTGACGACGACGCTGCCACTGGGAGACCAAGTCTATCTGTGCCAGGCG 2388
QY 601 GlnLysProSerAspArgAlaAspSerArgArgSerTyrHisGluGlnSerProPheGln 620
DB 2389 CAGAAACCAAGTACAGAGCTGACTCGCGCGAGCTGGCATAGAGAGACCCCTTTGAA 2448
QY 621 LysGlnPheLysArgArgSerCysGlnMetGluPheGlyGlnSerIleMetSerGluAsn 640
DB 2449 AAGCAGTTTAAAGCGAGAGCTGCCAAATGGAATTTGAGAGAGCATCATGTCAGAAAC 2508
QY 641 ArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetGlu 660
DB 2509 AGCTTACGGGAAGAGCTGGGAAAGTGGCAGTCACTTACTTTCCGGCAGCATGGAA 2568
QY 661 IleIleGluValSer 665
DB 2569 ATCATTCAGGCTCTCC 2583
RESULT 10
ADAS3105
ID ADAS3105 standard; cDNA; 2102 BP.
XX
XX
AC ADAS3105;
XX
XX
DT 20-NOV-2003 (first entry)
XX
XX
DE Human coding sequence, SEQ ID 673.
XX
XX
XX Cytosolic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
XX Gene Therapy; human; secretory protein; membrane proteins; cancer;
XX inflammatory disease; osteoporosis; neurological disease; gene; ss.
OS Homo sapiens.
XX
XX
PN BP1293569-A2.

XX PD 19-MAR-2003.
XX PF 21-MAR-2002; 2002EP-00006586.
XX PR 14-SEP-2001; 2001JP-00328381.
XX PR 24-JAN-2002; 2002US-0350435P.
XX PA (HELI-) HELIX RES INST.
XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,
XX PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Irie R, Tamechika I,
XX PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuko Y;
XX DR WPI; 2003-395539/38.
XX DR P-PSDB; ADA54744.
XX PT New polynucleotides encoding full-length polypeptides, e.g. secretory
XX PT and/or membrane proteins, useful for developing medicines for diseases in
XX PT which the gene is involved, or as target molecules for gene therapy.
XX PS Claim 1; SEQ ID NO 673; 205bp; English.
XX CC The present invention relates to novel human secretory or membrane
XX CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
XX CC ADA54071). The coding sequences are useful in the gene therapy of
XX CC diseases caused by abnormalities of the proteins, e.g. cancer,
XX CC inflammatory diseases, osteoporosis or neurological disease.
XX SQ Sequence 2102 BP; 542 A; 546 C; 510 G; 504 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 2102
Score: 3399.00 Matches: 662
Percent Similarity: 99.70% Conservative: 1
Best Local Similarity: 99.55% Mismatches: 2
Query Match: 99.44% Indels: 0
DB: 1 Gaps: 0

US-10-029-345A-109 (1-665) x ADA53105 (1-2102)
QY 1 MetAlaHisGluMetIleGlyThrGlnIleValaThrGluArgLeuValAlaLeuLeuGlu 20
DB 56 ATGGCCCATGAGATGATTTGGAATCTCAATTTACTGAGAGCTTGCGCTCTCTGAAA 115
QY 21 SerGlyThrGluValLeuLeuIleAspSerArgProPheValGluIleAsnThrSer 40
DB 116 AGTGAAGCGAAAAGTCTGCTAATTGATAGCCGGCATTTTGGAATACAAATACATCC 175
QY 41 HisIleLeuGluAlaIleAsnIleAsnGlySerIleuLeuMetIleValArgLeuGln 60
DB 176 CACATTTTGGAAAGCATTAATATCAACTGCTCAAGCTTATGAAGCAAGGTTCACAG 235
QY 61 AspValValLeuIleThrGluLeuIleGlnHisSerAlaValSerHisValAspIleAsp 80
DB 236 GACAAAGTGTAAATTAACAGACTCATCCAGCATTCAGGAAACATAAGTTGACATTGAT 295
QY 81 CysSerGluValValValIleValIleValIleValIleValIleValIleValIleVal 100
DB 296 TGCAGTCAGAAAGTTGATGTTACATCAAAAGCTCCCAAGATGTGCTCTCTCTTCA 355
QY 101 AspCysPheLeuThrValLeuLeuGlyValLeuGluIleValSerPheAsnSerValHisLeu 120
DB 356 GACGTGTTTTCACCTGTAATCTTGCTGGTAACTGGAGAAAGAGCTTCACTGTTCACCTG 415
QY 121 LeuAlaGlyValPheAlaGluPheSerArgCysPheProGlyLeuGluGluIleValSer 140
DB 416 CTTCAGAGTGGTGTGCTGAGCTCTCTGTTGTTTCCCTGGCCCTCTGGAAGAAATCC 475
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
DB 476 ACTCTAGTCCCTACCTCACTTTCAGACCTTGCTTACCTGTGCAACATTTGGGCCAAC 535

QY 161 ArgIleLeuProAsnLeuIleValLeuGlyCysGlnArgAspValLeuAsnGlyLeuIle 180
DB 536 CTAAATCTTCCCAATCTTTATCTTGCTGCCAGCGAGATCTCTCAACAAAGAGCTGATG 595
QY 181 GlnGlnAsnGlyIleGlyIleValLeuAsnIleSerThrCysProIleProAspPhe 200
DB 596 CAGCAGAAATGGATGGTATGTTGTTAAATGCCAGCAATACCTGTCCAAAGCCGTGACTTT 655
QY 201 IleProGluSerHisPheLeuArgValProValAsnAspSerThrCysGlyValIleLeu 220
DB 656 ATCCCAAGTCTCAATTTCTGCGTGTGCTGTAAATGACAGCTTTGTGAAAATTTTG 715
QY 221 ProTrpLeuAspIleValIleAspPheIleGluValAlaValIleAsnGlyCysVal 240
DB 716 CCGTGTGGACAAATAGTATGATTTTATGAGAAAGCAAAACCTCCAAATGATGTGTT 775
QY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaIleMet 260
DB 776 CTAGTGACATGTTTAGCTGGGATCTCCCGCTCCGACCATCGCTATCGCTATCATCATG 835
QY 261 LysArgMetAspMetSerLeuAspGluAlaIleValArgPheValIleGluValArgProThr 280
DB 836 AAGAGATGAGCATATGCTTTAGATGAAGCTTACAGATTTGTGAAGAAAAGAAAGCTTACT 895
QY 281 IleSerProAsnPheAsnPheLeuGluGlnLeuLeuAspTrpGluIleValAsn 300
DB 896 ATATCTCCAAATCTTCAATTTTCTGGGCCAACTCTGAGATATGAAAGAAAGATTAAAGAAC 955
QY 301 GlnThrGlyAlaSerGlyProIleValSerIleValLeuLeuHisIleGluIleValProAsn 320
DB 956 CAGACTGAGACATCAGGGCCAAAGAGCAAACTCAACCTCTGCACTGGAAGAGCCAAAT 1015
QY 321 GluProValProAlaValSerGluGluIleValSerGluThrProLeuSerProPro 340
DB 1016 GAACCTGCTCTCTCTCTCTCAAGAGGTGACAGAAAGAGAGAGGCTCTCACTCCACCC 1075
QY 341 CysAlaAspSerAlaThrSerGluAlaIleGluIleValIleValProValHisIleProAlaSerVal 360
DB 1076 TGTGCCACTGCTCTCACTCAGAGGACAGCAGCAAAAGCCCGTGTATCCCGCAGCGTG 1135
QY 361 ProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAlaLeu 380
DB 1136 CCCAGGTGCCAGCGCTGAGCGCTGCTGTAAAGAACAGCCCGTGTATCAGGGCTC 1195
QY 381 SerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnIleValArgSerPhe 400
DB 1196 AGTGGCTGCACCTGTCCCAAGACAGCTGGAAGACAGCAATAGCTCAAGCTTCTTC 1255
QY 401 SerLeuAspIleIleValSerValSerTrpSerAlaSerMetAlaIleSerLeuHisGlyPhe 420
DB 1256 TCTCTGATATCAATCAATTCATATTCAGCCAGCATGGCAGCATCTTATCATGGCTTC 1315
QY 421 SerSerSerGluAspAlaLeuGluIleValIleValProSerThrThrLeuAspGlyIleHis 440
DB 1316 TCTCATCAAGAAAGTCTTGAATATCAAAACCTTCCATCACTGTGATGAGCAAC 1375
QY 441 LysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSerPro 460
DB 1376 AAGCTATGCAAGTCTCCCTGTTTCAAGAACTATGAGAACACATCCCAAAACCACTCT 1435
QY 461 AspIleGluGluAlaSerIleProIleValLeuGlnThrAlaArgProSerAspSerGln 480
DB 1436 GATTAAGAGAGAGAGCAGCATCCCAAGAAAGCTGACAGACTGCAGAGCTTCAAGACG 1495
QY 481 SerLysArgLeuHisSerValAlaArgHisSerSerSerGlyThrAlaGlnArgSerLeu 500
DB 1496 AGCAAGCATTCATTCGTTGTTCAAGAACAGACAGATGGACCGCCCAAGAGTCCCTTTTA 1555
QY 501 SerProLeuHisArgSerGlySerValGluAspAsnTrpHisThrSerPheLeuPheGly 520
DB 1556 TCTCACTGCATCGAAGTGGAGGCTGAGAGCAATTAACACAGCTTCTTTTCCG 1615

Db	443	ACTCTAGTCCCTTACCTCGCATTTCTCAGCCTTGTACCTGTTACCTGTTGCCAACATTGGGCCAAC	502
QY	161	ArqllleleupProasnuLeuTyrlenglyCySglnaIrgasPValleuAsnlysgluleu	180
Db	503	CGAAATTCCTCCCAATCTTATCTTGGCTCGACGAGATGTCTCTCAACAAGAGCTGATG	562
QY	181	GlnGlnaenrglyIileglyTyValleuAsnAlaserTyTrThCyBProLyPProasPhe	200
Db	563	CAGCAGAAAGGGAATGGTATGTGTTAAATGGCAGCAAAATCTGTCCAAAGCCTCACTT	622
QY	201	IleProGlnSeSethPheLeuArgValProValAsnAspSerPheCysgluIlyslleu	220
Db	623	ATCCCGGAGTCTCATTTCTTCCGCTGTGCTGTGCAATGACAGCTTTTGTGAGAAAATTTTG	682
QY	221	ProTlPLeuAspLySerValAspPheIlegluIysAlaIyAsAlaSerAsnGlyCyVal	240
Db	683	CCGTGGTGGACAAATCAGTAGATTTTCATTGTGAAAGCAAAAGCCTCCCATGTGATGTGT	742
QY	241	LeuValHisCysLeuAlaaglyTlleSerArgSerAlaThrIleAlaIleAlaTyrlleMet	260
Db	743	CYAGTGCACTGTTTATGCTGGAGTCTCCCGCTCCGCGCACATGCGTATCGCTACATCATG	802
QY	261	LySArgMetAspMetSerLeuAspGluAlaTyArgPheValIySGluIySarPProTh	280
Db	803	AAAGAGATGACATGTCTTTAATGATGAAGCTTCAAGATTTGTGTAAGAAAAGAACTACT	862
QY	281	IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrgluIyIySAlleuYAsn	300
Db	863	ANATCTCCAAACTTCAATTTTCTGGGCCAACTCTGGACTATGAGAGAAGATTAAAGAC	922
QY	301	GlnThrGlyAlaSerGlyPProLySerIySleuIyLeuHisIySGluIySProAsn	320
Db	923	CAGACTGGAGCATCAAGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTGGAGAAAGCAAT	982
QY	321	GluPProValProAlaValSerGluGlyGlyGlyIySserGluThPProLeuSerProPro	340
Db	983	GAACCTGTCCCTGCTGCTCTCAAGAGGTGACAGAAAAGCAAGCCCTCAGTCCACCC	1042
QY	341	CysAlaAspSerAlaThrSerGlnAlaAlaGlyGlnArgProValHisProAlaSerVal	360
Db	1043	TCTGGCGACTCTGCTACCTCAAGGCAAGGAGCAAAAGCCCTGTGATCCGCGCAGCGTG	1102
QY	361	ProSerValProSerValGlnPProSerLeuLeuIyAsPSerProLeuValGlnAlaLeu	380
Db	1103	CCCAACGTGCCCAAGCGGTGACGCCGTGCTGTTAAGAGACAGCCCGCTGGTACAGCGCTTC	1162
QY	381	SerGlyLeuHisLeuSerIleAspArgIyGluIyAsPSerAsnIyLeuIySarSerPhe	400
Db	1163	AGTGGGCTGCACCTGTCCGCAACACAGGCTGTGAAGACAGCAAAATMACTCAAGGTTCTTC	1222
QY	401	SerLeuAspIleIySerValSerTyrselArgSerMetAlaAlaSerIyHisIyGlyPhe	420
Db	1223	TCTCTGGAATATCAATTCAGTTTCATTTTCAGCCACACATGCGACATCTTACATGGCTTC	1282
QY	421	SerSerSerGluAspAlaLeuGluIyTyTrIyIySProSerThrThLeuAspGlyThrAsn	440
Db	1283	TCTCATATCAGAAAGCTTTGGAAATACAAACCTTCCACTACATCTGGATGGACCAAC	1342
QY	441	LySLeuCySglnPheSerProValGlnGluLeuSerGluGlnThPProGluThSerPro	460
Db	1343	AAGCTATGCGAGTTCTCCCTCGTTTACAGAACTATGAGAGCAACATCCGAAACCGAGTCT	1402
QY	461	AspLySgluGluAlaSerIleProLySlySleuGlnThPAlaArgProSerAspSerGln	480
Db	1403	GATAAGAGAGAAAGCCAGCATCTCCCAAGAAAGCTGCAACCGCGAGGCTTTCAGACAGCCAG	1462
QY	481	SerIySarGlyLeuHisSerValArgThSerSerSerGlyThPAlaGlnArgSerIyLeu	500
Db	1463	AGCAAGCATTTGCATTCCGTGAGAACCAAGACAGCATGTGGACCGGCCCAAGGTCCTTTTA	1522
QY	501	SerPProLeuHisArgSerGlySerValGluAspAsnTyTrHisSerPheLeuPheGly	520
Db	1523	TCTCCACATGCATCGAAGTGGGAGCGTGGAGCAATTACACACACAGCTTCTTTTTCGGC	1582

QY	521	LeuserThrSerGlnGlnhIleuLeuThrIleSerAlaGlyIleuGlyLeuMetGlyTPRHis	540
Db	1593	CTTTCACCAACCCAGACACACTTACGAAAGCTGCTGGCTTGAGGCTGAC	1642
QY	541	SerAspIleuAlaProGlnThrSerThrProSerLeuThrSerSerTrpIyrPheAla	560
Db	1643	TCGGATATCTTGGCCCCCAGACCTTCAACCTTCCCTTGACCAAGCACTGGTATTTTGGC	1702
QY	561	ThrGlnSerSerHisPheTyrSerAlaSerAlaIleTyrGlySerAlaSerTyrSer	580
Db	1703	ACAGAGTCTTCACACTTCTACTCTGCTCCCTCAGCCATCTACCGAAGCAAGTGCAGTTACTCT	1762
QY	581	AlaTyrSerCysSerGlnIleuProThrCysGlyIAspGlnAlaTyrSerValArgArgArg	600
Db	1763	GCCATACAGCTGACACCACTGCCCCCACTTGGGAGAACCAAGCTTATTTGTGGCGAGCGG	1822
QY	601	GlnIysProSerAspArgAlaAspSerArgArgSerTrpHisGlnGlnSerProPheGln	620
Db	1823	CAGAAAGCCAAGTGCAGAGGCTGACTGCGCGGAGGCTGGCATGAAAGAACCCCTTTGAA	1882
QY	621	LysGlnPheIleValArgArgSerCysGlnMetGluPheGlyGlnSerIleMetSerGluAsn	640
Db	1883	AAGCAAGTTTAAACCCCAAGACTGCCCAATGGAAATTGGAGAGAGCAATCATGTACAGAAC	1942
QY	641	ArgSerArgGlnGlnIleuGlnGlyIleValGlySerGlnSerSerPheSerGlySerMetGlu	660
Db	1943	AGGTTCACGGAGAGAGCTGGGGGAAGTGGGAGTCACTAGCTTAGCTTTTGGGACAGATGGAA	2002
QY	661	IleIleGlnValSer	665
Db	2003	ATCATTTGAGGTCTCC	2017
RESURF_12			
ACC60521			
ID	ACC60521	standard; cDNA; 5111 BP.	
XX	ACC60521;		
AC			
DT	19-JUN-2003	(first entry)	
DE			
XX		Polynucleotide relating to the invention SEQ ID NO: 41.	
KW		Gene; ss; antiproliferative; hepatotropic; nephrotropic; antiarthritic;	
KW		antiproliferative; cardiac; cytostatic; gene therapy; liver disease;	
KW		proliferative disorder; renal failure; cardiovascular disorder;	
KW		immunological disorder; arthritis; psoriasis; congenital heart defect;	
XX		congestive heart failure; cancer; human; mouse; yeast; rat; fruitfly.	
OS		Homo sapiens.	
XX			
PN	WO200257460-A2.		
PD	25-JUL-2002.		
XX			
PF	20-DEC-2001; 2001WO-US050459.		
XX			
PR	20-DEC-2000; 2000US-0256868P.		
PR	30-MAR-2001; 2001US-0280186P.		
PR	01-MAY-2001; 2001US-0287735P.		
PR	05-JUN-2001; 2001US-0295848P.		
PR	25-JUN-2001; 2001US-0300465P.		
XX			
PA	(BRIM) BRISTOL-MYERS SQUIBB CO.		
XX			
PI	Jackson DG, Feder J, Nelson T, Mintier G, Ramanathan C, Lee L,		
PI	Siemens N, Bol D, Schieven G, Finger J, Todderick CG, Bassolino D;		
PI	Krystek S, Mcatee P, Suchard S, Banas D,		
XX			
DR	WPI; 2002-599721/64.		
XX			
DR	P-PSDB; ABR52352.		
XX			
PT	Novel polynucleotides encoding human phosphatase polypeptides useful in		

PT the prevention or treatment of e.g. proliferative and cardiovascular disorders.

XX Claim 1; Fig 5; 801pp; English.

XX The invention relates to a novel isolated nucleic acid comprising a polynucleotide having a nucleotide sequence selected from 40 polynucleotides fully defined in the specification. The polynucleotide of the invention has antiproliferative, hepatotropic, nephrotropic, CC antiarthritic, antiproliferative, cardiant, and cytostatic activity. The CC polynucleotide may have a use in gene therapy. A polynucleotide or CC polypeptide of the invention is useful for preventing, treating or CC ameliorating a medical condition, e.g. a proliferative disorder. They are CC also useful for treating e.g. liver disease, renal failure, immunological CC disorders including arthritis and psoriasis, cardiovascular disorders CC such as congenital heart defects and congestive heart failure, and CC cancer. A method of the invention is useful for diagnosing a pathological CC condition or susceptibility to a condition in a subject. The present CC sequence is used in the exemplification of the invention

XX Sequence 5111 BP; 1413 A; 1112 C; 1232 G; 1354 T; 0 U; 0 Other:

Alignment Scores:

Pred. No.: 0 Length: 5111
Score: 3388.00 Matches: 661
Percent Similarity: 99.55% Conservative: 1
Best Local Similarity: 99.40% Mismatches: 3
Query Match: 99.12% Indels: 0
DB: 1 Gaps: 0

US-10-029-345A-109 (1-665) x ACC60521 (1-5111)

QY 1 MetAlhIeGlnuMeIleGlyThrGlnIleValThrGlnArgLeuValAlaLeuLeuGlu 20
Db 470 ATGGCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 529
QY 21 SerGlyThrGlnuValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
Db 530 AGTGAAGCGGAAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 589
QY 41 HleIleLeuGlnuAlaIleAlaIleAlaIleAlaIleAlaIleAlaIleAlaIleAlaIle 60
Db 590 CACATTTTGAACCATTAATATCACTCCCAAGCTTGAAGCAAGCTTGAAGCAAGCTTGA 649
QY 61 AspLeuValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
Db 650 GACAAAGTGTAAATACAGAGCTATCAGCAATTCAGCAATTCAGCAATTCAGCAATTCAG 709
QY 81 CysSerGlnuValValValValValValValValValValValValValValValValVal 100
Db 710 TGCAGTCAGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 769
QY 101 AspCysPheLeuThrValLeuLeuGlyValLeuGlnuValSerPheAlaSerValHleu 120
Db 770 GACTGTTTCTCCTGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 829
QY 121 LeuAlaGlyValPheAlaGlnuPheSerArgCysPheProGlyLeuGlyValSerVal 140
Db 830 CTTCAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 889
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAlaIleGlyProThr 160
Db 890 ACTCTAGTCCCTACCTGCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 949
QY 161 ArgIleLeuProAlaLeuLeuValCysGlnArgAspValLeuAlaIleValLeuIle 180
Db 950 CGAATCTTCCCAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1009
QY 181 GlnGlnAlaGlnuValLeuValLeuAlaSerValThrCysPheProValPheAla 200
Db 1010 CACGAGATGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1069
QY 201 IleProGlnuSerIlePheLeuArgValProValAlaAlaPheSerPheCysGlyValLeu 220

Db 1070 ATCCCGAGCTCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1129
QY 221 ProThrLeuAlaPheSerValAlaPheIleGlyValAlaValAlaSerAlaGlyVal 240
Db 1130 CCGTGTGTGACAAATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1189
QY 241 LeuValHleCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaIleAlaIle 260
Db 1190 CTAGTCACCTGTTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1249
QY 261 LysArgMetAlaPheSerLeuAlaPheValAlaValAlaValAlaValAlaValAlaVal 280
Db 1250 AAGAGATGACATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1309
QY 281 IleSerProAlaPheAlaPheLeuGlyValLeuLeuAlaPheValLeuValLeuVal 300
Db 1310 ATATCTCCAAACTTCAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1369
QY 301 GlnThrGlyAlaSerGlyProLysSerValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 320
Db 1370 CAGACTGAGCATCAGGCGCCAAAGCAAACTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCT 1429
QY 321 GluProValProAlaValSerGlnuGlyValGlnuLysSerGlnuThrProLeuSerPro 340
Db 1430 GAACCTGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1489
QY 341 CysAlaAlaPheSerAlaThrSerGlnuAlaAlaGlyValArgProValHleProAlaSer 360
Db 1490 TGTGCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1549
QY 361 ProSerValProSerValGlnProSerLeuLeuGlnuAlaPheSerProLeuValGlnAla 380
Db 1550 CCAAGCTGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1609
QY 381 SerGlyLeuHleuSerAlaAlaPheArgLeuGlnuAlaPheSerAlaPheSerVal 400
Db 1610 AGTGGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1669
QY 401 SerLeuAlaPheLeuSerValSerValSerValSerValSerValSerValSerVal 420
Db 1670 TCTCTGATATCAAAATCAGTTTCAATTCATGACGACATGACATGACATGACATGAC 1729
QY 421 SerSerSerGlnuAlaLeuGlnuValValValValValValValValValValValVal 440
Db 1730 TCTCTATCAGAGATGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1789
QY 441 LysLeuCysGlnPheSerProValGlnuLeuSerGlnuGlnuThrProGlnuThrSerPro 460
Db 1790 AAGCTATGCAAGTTCCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1849
QY 461 AspLeuGlnuAlaSerIleProValValLeuGlnuThrAlaArgProSerAlaPheSerGln 480
Db 1850 GATTAAGAGAGAACCCAGATCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1909
QY 481 SerValArgLeuHleuSerValArgThrSerSerSerGlyThrAlaGlnuSerLeuLeu 500
Db 1910 AGCAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1969
QY 501 SerProLeuHleuArgSerGlySerValGlnuAlaPheValAlaIleAlaIleAlaIleAla 520
Db 1970 TCTCAGCTGATGAGATGAG 2029
QY 521 LeuSerThrSerGlnuGlnuAlaLeuThrValSerAlaGlyValLeuGlyValLeuPhe 540
Db 2030 CTTTCCACAGCAG 2089
QY 541 SerAspIleLeuAlaProGlnuThrSerThrProSerLeuThrSerSerThrProValPheAla 560
Db 2090 TCGGATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2149
QY 561 ThrGlnuSerSerIlePheValSerAlaIleValGlyValSerValSerValSerValSer 580

D	b		2150	ACAGAGNICTTCAACTTCTACTCTGCGCTCAGACCATTCAACGGAGGAGGCCAGTTACTCT	2208
O	y		581	AlaIyYserCySSergInLeuProThrCysGIyAapGIuValIYYSerValArgArgArg	600
D	b		2210	GCCTAACAGCTCACACCGAGCTGCCCTTGCGGAGCCAAGTCATYTCGTGCGCAGGC	2263
O	y		601	GIuIySProSeraBPARGAlaaSPSerArgArgsertPbHlsgIuIuSerProPhgInu	620
D	b		2270	CAGAA GCCAAGACAGAGCTGACTGCTCGCGCGAGACTGGCATGANGAGA GCCCTTTGA	2325
O	y		621	LysGIuPhelySArGARSerSerCysGIuMetGIuPhelGIyIuSerIlmeSerGIuAn	640
D	b		2330	AAGCAGTTTAAACGCAGAACGCTGCCAATVGAAATTGGAGAGAGCATCATGCAAGAAC	2389
O	y		641	ArgSerarvgIuGIuLeuGIyLysValGIySerGIuInserserPheserGIySernetGIu	660
D	b		2390	AGGTCACCGGAGAACGCTGGGGAAAGTGGGACAGTCAGTCTTAGCTTTGGGACGACATGAAA	2445
O	y		661	IleIIlegIuValSer 665	
D	b		2450	ATCATTGAGGTCTCC 2464	
RESULT 13					
A	F	3	0479	AAF30479	
I	D			AAF30479 standard; cDNA; 2118 BP.	
X	X			AAF30479;	
A	C				
X	X				
D	T			29-MAY-2001 (first entry)	
X	X				
D	E			Human protein phosphatase and kinase protein-4 CDNA I234795CB1.	
X	X				
K	M			Protein phosphatase and kinase protein; PPHK-4; human;	
K	M			gastrointestinal disorder; immune system disorder; neurological disorder;	
X	X			cell proliferative disorder; cancer; diagnosis; therapy; ss.	
O	S			Homo sapiens.	
X	X				
X	X				
F	H			Key Location/Qualifiers	
P	T			CDS 25..2025	
F	T			/tag= a	
F	T			misc_feature 163..222	
F	T			/tag= b	
F	T			misc_feature /note= "unique fragment"	
F	T			1081..1140	
F	T			/tag= c	
F	T			/note= "unique fragment"	
X	X				
P	N			WO200120004-A2.	
X	X				
X	X			22-MAR-2001.	
X	X				
P	F			14-SEP-2000; 2000MO-US025515.	
X	X				
P	R			15-SEP-1999; 99US-0154141P.	
X	X				
P	A			(INCY-) INCYTE GENOMICS INC.	
X	X				
P	I			Yue H, Tang YT, Bandman O, Hillman JL, Baughn MR, Azimzai Y,	
X	X			Lu DAM;	
X	X				
D	R			WPI; 2001-244811/25.	
D	R			P-P5DB; AAB20325.	
X	X				
P	T			Novel human protein phosphatase and kinase proteins for diagnosis,	
P	T			treatment and prevention of gastrointestinal, immune system, neurological	
P	T			and cell proliferative disorders.	
X	X				
X	X			Claim 5, Page 97-98, 103pp; English.	
X	X				
C	C			The present sequence is that of cDNA encoding novel human protein	
C	C			phosphatase and kinase protein PPHK-4 (see AAB20325). The cDNA was	
C	C			initially identified in Incyte Clone ID No. 1234795CB1, from a foetal	

CC	Lung tissue library.Tissues that express PPHK-4 (as a fraction of total
CC	tissues expressing PPHK-4) include gastrointestinal (0.385).
CC	cardiovascular (0.154), nervous (0.154) and reproductive (0.154).
CC	diseases or conditions associated with tissues expressing PPHK-4 (as a
CC	fraction of total tissues expressing PPHK-4) include cancer (0.692),
CC	inflammation or trauma (0.308) and cell proliferation (0.231). The
CC	encoded protein shows homology to mouse neuronal tyrosine threonine
CC	phosphatase 1. The invention provides human PPHK-1 to -11 polypeptides
CC	(see AAB20322-32) and polynucleotides (see AAF30476-86). It also provides
CC	expression vectors, host cells, antibodies, agonists and antagonists, as
CC	well as methods for diagnosing, treating or preventing disorders
CC	associated with expression of PPHK, including gastrointestinal
CC	disorders, immune system disorder, neurological disorders and cell
CC	proliferative disorders, including cancer
XX	
SQ	Sequence 2118 BP; 550 A; 552 C; 506 G; 510 T; 0 U; 0 Other;
Alignment Scores:	
Pred. No.:	0 Length: 2118
Score:	3373.00 Matches: 663
Percent Similarity:	99.40% Conservative: 1
Best Local Similarity:	99.25% Mismatches: 3
Query Matchn:	98.68% Indels: 1
DB:	Gaps: 0
US-10-029-345A-109 (1-665) x AAF30479 (1-2118)	
OY	1 MetAlAHtsgImEtIleGlyThrGlnIleValThrGluArgLeuValAlaleuLeuGlu 20
Dd	25 ATGGCCCATGAGATGATTGGAACTCAAAATTGTACTGAAGTTGGTGCCTCGCGGAA 84
OY	21 SerGIythrGluLysValleuLeuIleAspSerArgProPheValGlutyrAsnThrSer 40
Dd	85 AGTGAAACGSAAAAAGTCGCTGAATTGATTACCGGCCCATTTGTGGAAATACAATACATCC 144
OY	41 HisIleLeuGluAlaIleAsnIleAsnCyseSerLysMetLysArgArgLeuGlnGln 60
Dd	145 CACATTTTGGAAAGCCATTATAATCAACTGCTCCAAGCTTATAGAAGCGAAGTTGGCAACG 204
OY	61 AsplysValleuIleThrGluLeuIleGlnHisSerAlaLysHisLysValAspIleAsp 80
Dd	205 GACAAAGTGTTAATTACAGAGCTCATCCGACATTACGCAAAACATTAAGTTGACATTGAT 264
OY	81 CySserGlnLysValValValtyrAspGlnSerSerGlnAspValAlaserLeuSerSer 100
Dd	265 TGCAGTCAGAAGGTGTGATTACATCAAACCTCCGAAGATGTGCCTCTCTCTTCA 324
OY	101 AspCysPheLeuThrValleuLeuGlyLysLeuGluLysSerPheAsnSerValHisLeu 120
Dd	325 GACGTGTTTTCTACTGTACTTCTGGGTAAACTCGAGAAAGCTTCAACTCTGTTACCTG 384
OY	121 LeuAlagLyPheAlagLuPheSerArgCysPheProGlyLeuCysGluGlyLysSer 140
Dd	385 CTTCAGAGGGGTGGTCTGAGTTCTCTCGTTGTTTCCCTGGCCCTCGTGAAGGAAATCC 444
OY	141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
Dd	445 ACTCTAGTCCCTCACTGCACTTCTCAAGCTTGCTTACCCTGTCCAACATTGGGCCAAC 504
OY	161 ArgIleLeuProAsnLeuTyrcLeuGlyCysGlnArgAspValleuAsnLysGluLeu 180
Dd	505 CGAATTCTTCCCAATCTTATCTTGGCTCCGACGAGATGTCTTCAACAAGAGCGTAGT 564
OY	181 GlnGlnAsnglyITilegLYrValleuAsnAlaserTYrThrCysProLysProAspPhe 200
Dd	565 CAGCAGAAAGGAGATGGTATGTATGTTAAATGCCAGCAATACCTGTCCAAAGCTGACTTT 624
OY	201 IleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGluLysIleLeu 220
Dd	625 ATCCCCGAGTTCATTTCTCGCGTGGCTGTGAATGACAGCTTTGTGAGAAATTTTG 684
OY	221 ProTPLeuAspLysSerValAspPheIleGluLysAlaLysAlaserAnglyCysVal 240

Db 685 CCGTGGTGGACAAATCATAGATTTTCATTGAGAAAAGCAAGCTTCAATGATGTGT 744
Qy 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaIleMet 260
Db 745 CTAGTGACATGTTAGTGGGATCTCCCGCTCCGCCACCATCGCTATCGCTACATATG 804
Qy 261 LysArgMetAspMetSerLeuAspGluAlaIleArgPheValIleGlyIleValSerProThr 280
Db 805 AAGAGATGACATGCTTTAGATGAGCTTACAGATTTTGGAAGAAAAAGAAAGCTACT 864
Qy 281 IleSerProAsnPheAsnPheLeuGlyIleLeuLeuAspIleGlyIleValIleValAsn 300
Db 865 ATATCTCCAACCTCAATTTTCTGGGCAACTCTTGACATATGAGAAAGATTTAAACAC 924
Qy 301 GluThrGlyAlaSerGlyProLysSerLysLeuLeuLeuLeuIleGluGlyIleValProAsn 320
Db 925 CAGACTGGAGCATTCAGGAGCAAGAGCAAACTCAAGCTGCTGCACTGGAGAAAGCAAT 984
Qy 321 GluProValProAlaValSerGlyIleGlyIleLysSerGluThrProLysSerPro 340
Db 985 GAACGTGCTCCCTGCTGCTCAGAGGGTGAAGAGAAAGCAAGAGCCCTCAGTCCAGCC 1044
Qy 341 CysAlaAspSerAlaThrSerGluAlaAlaGlyIleArgProValHisProAlaSerVal 360
Db 1045 TGTGCGACTCTGCTACCTCAGAGGAGAGCAAGAAAGCCGCTGATCCCGCAGCGCTG 1104
Qy 361 ProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAlaLeu 380
Db 1105 CCAGCGCTGCCAGCGTGCAGCCGCTGCTTGAAGAGACGCCGCTGGTACAGGCCCTC 1164
Qy 381 SerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLysSerPhe 400
Db 1165 AGTGGCTGCACCTGCTCCGAGAGAGGCTGGAAGACAGCAATAGCTCAAGCCGTCTTC 1224
Qy 401 SerLeuAspIleLysSerValSerIleSerAlaSerMetAlaAlaSerLeuHisGlyPhe 420
Db 1225 TCTGTGATATCAAAATCATGTTATTCATATTCAGCCAGCATGTGCATCTTACATGCTTC 1284
Qy 421 SerSerSerGluAspAlaLeuGluIleValIleValProSerThrThrLeuAspGlyThrAsn 440
Db 1285 TCTCTCATCAGAAATGCTTTGAACTACTCAAACTTCCACTCTCTGGAGTGGAGCAAC 1344
Qy 441 LysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSer-P 460
Db 1345 AAGCTATGCGAGTCTCCCTGTTCAAGAACTATCGAGAGAGACTCCCGAAACAGTTC 1404
Qy 460 LysAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSerAspSerG 480
Db 1405 CTGATATGAGGAGAGAGCAGCATCCCAAGAAAGCTGCAGACCGCCAGCGCTTCAGACAGCC 1464
Qy 480 InsSerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeu 500
Db 1465 AGAGCAAGCAGATTCATTCGCTCAGAACAGCAGCAGTGCACCGCCCAAGGTCCTTT 1524
Qy 500 euSerProLeuHisArgSerGlySerValGluAspAsnIleIleThrSerPheLeuPheG 520
Db 1525 TATCTCAGCTGATCGAAGTGGAGGCTGAGGAGCAATTACCAACAGCTTCTTTTOS 1584
Qy 520 LysLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyIleLysGlyIle 539
Db 1585 GCCTTTCCACACACAGCAGCAGCAGCTCAGAACTGCTGCGCGGCGCTTAAGGCGCTG 1644
Qy 540 HisSerAspIleLeuAlaProGlnThrSerThrProSerLeuHisSerSerThrPhe 559
Db 1645 CATTCGATATCTTGGCCCCCAAGACCTTACCCCTTCCCTGACAGCAGCACTGATTTT 1704
Qy 560 AlaThrGluSerSerHisPheThrSerAlaSerAlaIleIleGlyIleSerAlaSerIle 579
Db 1705 GCCACAGAGCTTCACACTTCTACTGCTCAGGCATTCACGAGGCAAGTGCAGATTAC 1764
Qy 580 SerAlaIleSerCysSerGlnLeuProThrCysGlyIleAspGlnValIleSerValArgArg 599
Db 1765 TCTGCTTACAGCTGACGCGAGCTGCGCACTTGGGAGAGCAAGTCTATCTGTGGCGCAGG 1824

Qy 600 ArgGlnLysProSerAspArgAlaAspSerArgSerTrpHisGluIleSerProPhe 619
Db 1825 CGGCAAGAGCAAGTACAGAGCTGACTCGCGCGAGCTGCGCATGAAAGAGACCTTT 1884
Qy 620 GluLysGlnPheLysArgArgSerCysGlnMetGluPheGlyIleSerIleMetSerGlu 639
Db 1885 GAAAGCAGTTTAAAGCAGAGAGCTGCCAATGGAATTTGAGAGAGCATCATGTCAAG 1944
Qy 640 AsnArgSerArgGluIleGluLeuGlyIleValGlyIleSerGlnSerSerPheSerGlySerMet 659
Db 1945 AACAGTCAAGGAGAGAGCTGGGAGAAAGTGGGAGTCAGTCACTTGTGGGAGCAGCATG 2004
Qy 660 GluIleIleGluValSer 665
Db 2005 GAATATCTTGAAGTCTCC 2022
RESULT 14
ACC60560
ID ACC60560 standard; cDNA; 2756 BP.
AC ACC60560;
XX 19-JUN-2003 (first entry)
DT 19-JUN-2003 (first entry)
XX
DE Polynucleotide relating to the invention SEQ ID NO: 113.
XX
KW Gene; ser; antiproliferative; hepatotropic; nephrotropic; antiarthritic;
KW antiproliferative; cardiant; cyostatic; gene therapy; liver disease;
KW proliferative disorder; renal failure; cardiovascular disorder;
KW immunological disorder; arthritis; psoriasis; congenital heart defect;
KW congestive heart failure; cancer; human; mouse; yeast; rat; fruitfly.
XX
OS Mus musculus.
XX
PN WO200257460-A2.
XX
PD 25-JUL-2002.
XX
PF 20-DEC-2001; 2001MO-US050459.
XX
PR 20-DEC-2000; 2000US-0256688P.
XX
PR 30-MAR-2001; 2001US-0280186P.
PR 01-MAY-2001; 2001US-0287735P.
PR 05-JUN-2001; 2001US-0295848P.
PR 25-JUN-2001; 2001US-0300465P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Jackson DG, Feder J, Nelson T, Mintier G, Ramanathan C, Lee L;
PI Stiemers N, Bol D, Schieven G, Finger J, Todderud CG, Bassolino D;
PI Krystek S, Mcatee P, Suchard S, Bannas D;
XX
XX MPI; 2002-599721/64.
DR P-PDB; ABR52385.
XX
PT Novel polynucleotides encoding human phosphatase polypeptides useful in
PT the prevention or treatment of e.g. proliferative and cardiovascular
PT disorders.
XX
PS Disclosure; Fig 16; 801pp; English.
XX
XX The invention relates to a novel isolated nucleic acid comprising a
XX polynucleotide having a nucleotide sequence selected from 40
XX polynucleotides fully defined in the specification. The polynucleotide of
XX the invention has antiproliferative, hepatotropic, nephrotropic,
XX antirhectic, antiproliferative, cardiant, and cyostatic activity. The
XX polynucleotide may have a use in gene therapy. A polynucleotide or
XX polypeptide of the invention is useful for preventing, treating or
XX ameliorating a medical condition, e.g. a proliferative disorder. They are
XX also useful for treating e.g. liver disease, renal failure, immunological
XX disorders including arthritis and psoriasis, cardiovascular disorders
XX such as congenital heart defects and congestive heart failure, and

CC cancer. A method of the invention is useful for diagnosing a pathological
CC condition or susceptibility to a condition in a subject. The present
CC sequence is used in the exemplification of the invention
XX
SQ Sequence 2756 BP; 714 A; 675 C; 664 G; 703 T; 0 U; 0 Other;

Alignment Scores:

Score:	0	Length:	2756
Percent Similarity:	3057.50	Matches:	594
Best Local Similarity:	93.68%	Conservative:	29
Query Match:	89.32%	Mismatches:	37
	89.45%	Indels:	5
		Gaps:	3

US-10-029-345a-109 (1-665) x ACC60560 (1-2756)

```
QY 1 MchahisgluWetiieglyThrglnlevalThrgluargleuValAlaleuenglu 20
Db ATGCCCATGATGATGTGMACTCAATTTGTACTGAGAGCTTGCTGCTGCGAA 428
QY 21 SerGlyThrgluValleuLeuileasSerArgProPheValGluTyraPheThrSer 40
Db AGTGAACGGAAGAGCTGCTAATGATGACGACCATTTGTGGAATCAATACGCT 488
QY 41 HisleuengluAlaleasnleasnCysSerlyseuWetlysaArgleuGln 60
Db CACATTTGAAACCATTAATATCACTGCTCCAACTGATGAAGCCAAAGCTTCAACG 548
QY 489 AspIysValleuilethrgluLeuileglnhisSerAlalyshislyseValAspIleAsp 80
Db GACAAAGTATTAATTAACGACTAATCAACCAATCTCAAAAGCAATAGGTGACATTGAC 608
QY 61 CysSerGlnlysaValValTyraSpGlnSerSerGlnAspValAlaserleuSerSer 100
Db TGCAATCAAAAGAGAGTATGATGATCAAGTTTCAAGATGTTGCTTCTGCTGCTCA 668
QY 609 AspCysPheleuThrValleuengluYlyseuGlnlysaSerPheasnSerValhisleu 120
Db GACTGCTTTCTCACTGACTTCTGGGTAAAGCTGAGAGAACCTTCAACTGCTCCACTG 728
QY 121 LeuAlaglyGlyPheAlGlnPheSerArgCysPheProGlyLeuCysGlnGlyLysSer 140
Db CTGGAGGTGCTTGTGAGAGTCTCTGTTGTTCCCTGGCTCTTGGAAGAAAGTCC 788
QY 729 ThrleuValProThrCysIleSerGlnProCysleuProValAlaAsnIleGlyProThr 160
Db ACTGAGTCCCTACTGCAATCTCAAGCTTCTTACTGCTGCGAACTGGGCAACT 848
QY 141 ArgIleleuProasnleuTyrlenglyCysGlnArgAspValleuasnlysgluLeuile 180
Db CGAATTTCTCCCAATCTCATCTTGGCTGCCAGAGATGTCCTCAACAAGAACCTGATG 908
QY 849 GlnGlnasnGlyIleGlyTyraValleuasnAlaserTyraThrCysProlyProAspPhe 200
Db CAACGAATGGGATGGCTATGTGTAAATGCAACCAATACCTGTCAAAGCTGACTTC 968
QY 909 IleProGlnSerHisPheleuArgValProValaAspSerPheCysGlnlyseIleleu 220
Db ATACTGTAATCTCACTTCTGCTGAGATGCTGGAATGACAGCTTTGTGGAAGAAATCTTA 1028
QY 969 ProTyrleuAspIysSerValAspPheIleGlylysaIlysaIleSerasnlyCysVal 240
Db CCATGCTGGACAAAGTCTGTGATTTCAATTGAGAAAGCAAAAGCCCTCAATGGCTGTGTG 1088
QY 1029 LeuValhisCysleuAlaglyIleSerArgSerAlaThrIleAlaIleAlaTyrlleMet 260
Db CTATTCACCTGCTTATGCTGAGATCTGCTGCTGCGACATATGCTATGCTCACTAC 1148
QY 1089 LysArgMetAspMetSerleuAspGlnAlaTyraPheValleuGlyLysArgProThr 280
Db AAGAGATGAGACATGCTCTTATAGAGCTTACAGATTTGTGAAGAAAGAAAGCACTACT 1208
QY 1149 ArgSerArgGlnGluLeuGlyValGlySerGlnSerPheSerGlySerMetGlu 660
Db 11SerProasnPheasnPheleuGlyGlnleuLeuAspTyraGlyLysIleLysAsn 300
```

```
Db ATATCCCGAATTTTATTTTATGGCCCAATCATGAGTATGAGAAAGCATTTAATAAC 1268
QY 301 GlnThrglyAlaserGlyProlySerlyseuIlyseuLeuNIleuGlnlysaProasn 320
Db CAGACTGGAATGCAAGGCGCAAGAGCAATGAAAGTCTGTGACTTGAACAAGCCACT 1328
QY 321 GluProValProAlaValserGlnGlyGlnIlyseuSerGlnlysaProleuSerProPro 340
Db GAGCCGCTGCTGCAACCTCAAGAGGCGATGGAAGAGTCACTGCTGATCAAGCCACC 1388
QY 341 CysAlaAspSerAlaThrSerGlnAlaAlaglyGlnArgProValhisProAlaserVal 360
Db TGTGCCAACTCG---ACCTCGAGGATCATAGGCAAGGCTTGTGCATCTTGA----- 1439
QY 361 ProSerValProSerValGlnProSerleuLeuGluAspSerProleuValGlnAlaleu 380
Db 1440 ---AGTGTCCCGCTTACAGCCGTCACTTGAAGACAGTCCGCTGATCAAGGCGCTC 1496
QY 381 SerGlyLeuNIleuSerAlaAspArgleuGluAspSerAsnlysaLeuLysArgSerPhe 400
Db AGTGGCTCCAGCTGCTTCAAGAACTGAAAGACAGACATTAAGCTCAAGCCTTCTTC 1556
QY 401 SerleuAspIleLysSerValSerTyraAlaserMetAlaAlaserleuNIleGlyPhe 420
Db TCTCTGATATCAAACTGTTTCATATTCAGCCAGATAGGCGCGCTTCTTCAACGGCTTC 1616
QY 421 SerSerSerGlnAspAlaleuGlnTyraTyraPheProSerThrThrleuAspGlyThrAsn 440
Db 1617 ---TCGTACAGAGAGGCTTTAGACTAGTCAAGAGTATCAGAAAGAGTCCAGAGCCAG 1673
QY 441 LysleuCysGlnPheSerProValGlnGluLeuSerGlnGlnThrProGlnThrSerPro 460
Db 1674 AAGCTTGCCAGATTCTCCCGCTTCAAGAGTATCAGAAAGAGTCCAGAGCCAGCCG 1733
QY 461 AspIysGlnGluAlaserIleProlysaLeuGlnThrAlaArgProAspSerGln 480
Db 1734 GATTAAGAGAGGCCCAATCCCAAGAGCCCAAGCTTCCAGGCTTTGAGAGCCAG 1793
QY 481 SerlysaArgleuNIleSerValArgThrSerSerSerGlyThrAlaGlnArgSerleu 500
Db 1794 GTCAAGCTTGGCACTAGTGAAGAACCGGAGTATGCGGCCAACCCAGAGCCCTTCTTC 1853
QY 501 SerProleuNIlsargSerGlySerValGluAspAsnTyraThrSerPheleuPheGly 520
Db 1854 TCGGCATGATCGAGCGGAGGTGTAAGAGCAATTAACAATCACTCTCTTTTGGC 1913
QY 521 LeuSerThrSerGlnGlnNIleuThrLysSerAlaglyleuGlyleuLysGlyTyraPhe 540
Db 1914 CTTTCCACAGCCAGCAACCTTCAACAGTCTGAGGCTTGGCTCAAGGCGCTGGCAC 1973
QY 541 SerAspIleleuAlaProGlnThrSerThrProSerleuThrSerSerTyraPheAla 560
Db 1974 TCAATATTTCTGGTCCCAAGTCTCTGCCCCCTCCCTGACAGACAAATGTGATTTTGGCT 2033
QY 561 ThrGlnSerSerHisPheTyraSerAlaIleTyraGlySerAlaserTyraSer 580
Db 2034 ACGGAGCCTTCACTTGTACTGCTTCAAGCACTTAAGAGCAACAGAGATTACTCT 2093
QY 581 AlaTyraSerCysSerGlnleuProThrCysGlyYsaPspGlnValTyraSerValArgArg 600
Db 2094 GCCTACAGCTGTGGCCAGCTGCGCCACTTGCAGTGAACCAAAATCTTGTTCGTAAGCGG 2153
QY 601 GlnLysProSerAspArgAlaAspSerArgArgSerTyraHisGlnGluSerProPheGlu 620
Db 2154 CAGAAGCTTACTGACAGAGCTGACTCGAGCGGAGCTGCGCATGAAAGAGGCCCTTTGAA 2213
QY 621 LysGlnPheLysArgArgSerCysGlnMetGlnPheGlyGlnSerIleMetSerGlnAsn 640
Db 2214 AAGCAGTTTAAACCAAGAGCTGCCAATGGAATTTGAGAGCACTTAATGTCCGAGAAC 2273
QY 641 ArgSerArgGlnGluLeuGlyValGlySerGlnSerPheSerGlySerMetGlu 660
```


DB 2274 AGGTCCAGGAGGAGCTGGGCAAGTGCGACGACGCTTCCGCGACGATGAG 2333
QY 661 |||||IleGluValSer 665
DB 2334 ATCATCGAGGCTCT 2348
RESULT 15
ABK48378
ID ABK48378 standard; cDNA; 3332 BP.
AC ABK48378;
XX
XX 02-JUL-2002 (first entry)
DE cDNA encoding human DSP-16 alternative form protein.
XX
XX Human; dual-specificity phosphatase-3; DSP-16; autoimmune disease;
KW mitogen-activated protein kinase; MAP; Duchenne muscular dystrophy;
KW cancer; graft-versus-host disease; allergy; metabolic disease;
KW abnormal cell growth; abnormal cell proliferation; contact inhibition;
KW cell cycle abnormality; anchorage independent cell growth; apoptosis;
KW intercellular adhesion; DSP-16 modulator; chromosome 12p; gene; se.
XX
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS /tag= a /product= "Human dual-specificity phosphatase-3 (DSP-16)
FT alternative form protein"
PN MO200226997-A2.
PD 04-APR-2002.
XX
XX 25-SEP-2001; 2001WO-US030124.
XX
XX 26-SEP-2000; 2000US-0235487P.
PR
XX (CEPT-) CEPTYR INC.
PA Luche RM, Wei B;
PI
XX
XX WPI; 2002-315802/35.
DR P-PSDB; AAU79159.
XX
XX New DSP-16 polypeptide, useful for identifying modulators of its
PT activity, which can be used in the treatment of disorders such as
PT Duchenne muscular dystrophy, or cancer.
XX
XX Claim 56; Fig 3; 87pp; English.
XX
XX The present invention relates to a new polypeptide, DSP-16, having a 665
CC amino acid sequence, given in the specification, or a variant having at
CC least 50 % identical residues, which retains the ability to
CC dephosphorylate an activated mitogen-activated protein (MAP) kinase. The
CC invention can be used for identifying agents which modulate DSP-16
CC activity, for modulation of a proliferative response in a cell, survival
CC of a cell, or differentiation of a cell. The cell displays contact
CC inhibition of cell growth or anchorage independent growth and may display
CC altered intercellular adhesion. The agent may modulate apoptosis, or the
CC cell cycle. The identified modulators can be used to treat Duchenne
CC muscular dystrophy, cancer, graft-versus-host disease, autoimmune
CC diseases, allergies, metabolic diseases, abnormal cell growth, abnormal
CC cell proliferation, and cell cycle abnormalities. The present nucleic
CC acid sequence is that of the human dual-specificity phosphatase-3 (DSP-
CC 16) gene located on chromosome 12p. This sequence encodes the human DSP-
CC 16 alternative form protein of the invention
XX
XX Sequence 3332 BP; 909 A; 805 C; 823 G; 795 T; 0 U; 0 Other;
Alignment Scores: 0 Length: 3332
Pred. No.:

Score: 3048.50 Matches: 607
Percent Similarity: 91.44% Conserved: 2
Best Local Similarity: 91.14% Mismatches: 1
Query Match: 89.19% Indels: 56
DB: 1 Gaps: 1
US-10-029-345A-109 (1-665) x ABK48378 (1-3332)
QY 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgGluValAlaLeuGlu 20
DB 562 ATGGCCCATGAGATGATGGAACTCAATTTGTTACTGAGAGGTTGGGCTCTGGGAA 621
QY 21 SerGlyThrGluValLeuLeuIleAspSerArgProPheValGluTyraThrSer 40
DB 622 AGTGAACGGAAATAAGTCTGCTAATTGATAGCCGGCACTTTGTGGAATACATCTCC 681
QY 41 HisIleGluGluAlaIleAsnIleAsnCysSerLysLeuMetLysArgArgLeuGln 60
DB 682 CACATTTTGGAAAGCCATTATATCACTGCTCCAGCTTATGAAGCGAAGTTGCAACAG 741
QY 61 AspLysValLeuIleThrGluLeuIleGlnHisSerAlaLysHisLysValAspIleAsp 80
DB 742 GACAAAGTGTAAATACAGAGCTCATCCAGCATTCAGCGAAACATTAAGTTGACATTGAT 801
QY 81 CysSerGlnLysValValValTyraAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
DB 802 TGCAGTCAGAAAGTTGATGTTACGATCAAAAGCTCCCAAGATGTGCTCTCTCTCA 861
QY 101 AspCysPheLeuThrValLeuLeuGlyLysLeuGluLysSerPheAsnSerValHisLeu 120
DB 862 GACTGTTTCTCACTGACTTCTGGGTAACCTGGAGAAAGACTTCAACTCTGTTCACTG 921
QY 121 -LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuGluGlyLys 140
DB 922 CTGG----- 925
QY 140 rThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProth 160
DB 925 ----- 925
QY 160 rArgIleLeuProAsnLeuTyrluGlyCysGlnArgAspValLeuAsnLysGluLeu 180
DB 926 -----CAGAGCTGAT 936
QY 180 eGlnGlnAsnGlyrIleGlyTyrrValLeuAsnAlaSerTyrrThrCysProLysProAsp 200
DB 937 GCAGCAGAAATGGATGTTATGTATGTAATGACAGCAATATCTGTCCAAGCCTGACTT 996
QY 200 eileProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluLysIle 220
DB 997 TATCCCGAGTCTCATTTCTGCGTGTGCTGTGATGACAGCTTTGTGAGAAATTTT 1056
QY 220 uProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAsnGlyCysVal 240
DB 1057 GCGGTGTTGACAAATACATGATGATTTCAATTGAGAAAGCAAGCCCAATGATGTGT 1116
QY 240 IleValHisCysLeuAlaGlyLysSerArgSerAlaThrIleAlaIleAlaTyrlle 260
DB 1117 TCTAGTGCACTGTTTAGCTGGGATCTCCGCTCCGACCATGCTATTCCTTACATCAT 1176
QY 260 tLysArgMetAspMetSerLeuAspGluAlaTyrrArgPheValIleGluLysArgProth 280
DB 1177 GAAGAGATGACATGCTTTTAAATGAAGCTTACAGATTTGTGAAGAAAGAAAGACCTAC 1236
QY 280 rIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrrGluLysIleLysAs 300
DB 1237 TATATCTCCAAACTCAATTTCTGGGCGCAACTCTGGAATATGAGAAAGAAATTAA 1296
QY 300 ngInThrGlyAlaSerGlyProLysSerLysLeuLysLeuHisGluGluLysProAs 320
DB 1297 CCAGACTGGAGCATCGAGGCCAAAGCAAACTCAAGCTGCTCACCCTGGAGAAAGCCAAA 1356
QY 320 ngIuProValProAlaValSerGluGlyGlnLysSerGluThrProLeuSerProPr 340

Db 1357 TGAACCTGTCCTGCTGCTCAGAGGAGTGGACAGAAAACGAGACGCCCTCAGTCCACC 1416
QY 340 oCYsAlaaspSerAlaThrSerGluAlaIaIyGlnArgProValHisProAlaSerVa 360
Db 1417 CTGTGCGGACTGCTGCTACTCAGAGGACAGAGGACAAAGGCCGTGATCCGCGAGCGT 1476
QY 360 lProSerValProSerValGlnProSerLeuLeuGluuAspSerProLeuValGlnAla 380
Db 1477 GCCCAGCGTGCCAGCGGTGACGCGCTGCTTAAAGAGACAGCCGCGTGTAAGCGCGCT 1536
QY 380 uSerGlyLeuHisLeuSerAlaAspArgLeuGluuAspSerLeuValGlyValArgSerPh 400
Db 1537 CAGTGGGCTGACCTGCTCCGACACGCGTGGAAGACAGCAATTAAGCTCAAGCGTCTT 1596
QY 400 eSerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPh 420
Db 1597 CTCTCGAGATCAATCAATGATTTCATATTCAACCGACATGGACGATCTTTCATGGCTT 1656
QY 420 eSerSerSerGluAspAlaLeuGluuTyrTyrLysProSerThrThrLeuAspGlyThrAs 440
Db 1657 CTTCCTATCAGAAAGATGCTTTGAAATACTACAAACCTTCCACTCTTGATGGGACCA 1716
QY 440 nLysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSerPr 460
Db 1717 CAAAGCTATGCCAGTTCTCCCTGTTCAAGAACTATCGAGACGAGACTCCCGAAACCAATCC 1776
QY 460 oAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSerAspSerG 480
Db 1777 TGATTAAGAGAGAAAGCCAGCATCCCAAGAGCTGCAGACCGCGAGCTTTCAGACAGCCA 1836
QY 480 nSerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeu 500
Db 1837 GAGCAAGGATTTGCTTGTGTCAGAACCAAGAGAGTGGCACCGCCAGAGGTCCCTTTT 1896
QY 500 uSerProLeuHisArgSerGlySerValGluuAspAsnTyrHisThrSerPheLeuPheG 520
Db 1897 ATCTCCACTGCATCGAAGTGGAGAGGTGGAGGACAAATTACACACAGCTTCTTTTCGG 1956
QY 520 yLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLysGlyTyrPh 540
Db 1957 CTTTCCACGAGCCGACGACCTTCACGAACTGTGCTGGCTGGGCTTAAAGGCTGGCA 2016
QY 540 sSerAspIleLeuAlaProGluThrThrSerThrProSerLeuThrSerSerTyrPheAl 560
Db 2017 CTCGGATATCTTGGCCCCCAGACCTTCAACCTTCCCTGACGAGCTGGTATTTTGC 2076
QY 560 aThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAlaSerTyrSe 580
Db 2077 CACAGAGTCTCACACTTCTACTCTGCTCAGCCATCTACGAGAGCAGTGCAGTTACTC 2136
QY 580 fAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArgAr 600
Db 2137 TGCCACAGCTGCGACGACGCTGCCACTTGGGAGACCAAGTCTATTCTGTGCGCAGGCG 2196
QY 600 gGlnLysProSerAspArgAlaAspSerArgArgSerTyrHisGluGluSerProPheG 620
Db 2197 GCAGAAAGCAAGTACAGAGGTGACTCGCGCGGAGCTGGCATGAAAGAGAGCCCTTGA 2256
QY 620 uLysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerIleMetSerGluAs 640
Db 2257 AAAGCAGTTTAAACGAGAAAGCTGCCAAATGGAATTGAGAGAGCATCATGTCAAGAA 2316
QY 640 nArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetG 660
Db 2317 CAGGTCAAGGAGAGAGCTGGGAGAAAGTGGCAGTCAGTCTTTCGGGCGACATGGA 2376
QY 660 uIleIleGluValSer 665
Db 2377 AATCATTAAGTCTCC 2392

Job time : 77 secs